musca domes

rattus norv

bos taurus

P15257 P32592 P54259

homo sapien sapien

rattus norv

Q01778 P25304 Q99466

homo sapien

drosophila

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Q9h091

sapien rattus norv epstein-bar sapien

homod

Q9w0k7 P51825 Q9nzm4 P55067 O15353

homo sapien

sapien

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P03181 Q9y2n3 Q15370

drosophila

062541 Q60974 261315

mus musculu mus musculu

homo sapien homo sapien mus musculu homo sapien rattus norv

000512 09ul36

Q9r187

mus musculu

Q9nrj4 P08921

rattus norv

drosophila

P54269

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
MEDLINE=96051387; PubMed=7584026;
NOMURA N., Mayajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D25539; BAA05022.1; -.
EMBL; Z99715; -2816670.1; -.
Hypotherical protein.
SEQUENCE 153 AA; 17035 MW; CAC3FBAF16821935 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AA
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                                                                                                                                                       AF4 HUMAN
GSR1 HUMAN
PGCN RAT
FXN1 HUMAN
YHL1 EBV
                HNFA RAT
ITB2 BOVIN
DRPL HUMAN
                                                                                     AGRI_RAT
NTC4_HUMAN
                                                                                                                                                                                                                                                                                 HUNB_DROYA
NCR1_MOUSE
APC_MOUSE
BCL9_HUMAN
Z236_HUMAN
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                                                                      HUNB MUSDO
                                                                                                                        HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                            LUL4 HUMAN
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NCBI_TaxID=9606;
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Q15053;
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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USFTO spool_p/USIO77682/runat_21092004_133240_20767/app_query.fasta_1.4615
-DE=SwissProt_42_-QFWT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USGR=USIO776827_@CGN 1 1 1.20 @runat_21092004_133240_20767 -MCDU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPENOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Compugen Ltd.
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           version
                                                                                                                  September 21, 2004, 15:06:11
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V70K_TYMVC
HNFA_HUMAN
V70K_OYMV
SAL2_HUMAN
ALC1_GORGO
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SAL2_MOUSE
APC_HUMAN
MUC2_HUMAN
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MUCZ HUMAN
NTC4 MOUSE
ALC1 HUMAN
SMOO HUMAN
APC RAT
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
            GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
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                                                                                                                                                                                                                                                                                                   PIR; A94062; RWRB.
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR007139; Ig_cl.
Pfam; PF00047; ig; 1.
SWART; SW00407; IG_like.
InterPro; IRE PS00815; Ig_like.
InterPro; IRE PS00815; Ig_like.
InterPro; Immunoglobulin domain; Transmembrane; Glycoprotein.
                                                                                                                                                                                                             AIGCACTAIGTCCAIGTCCACAGAGTAACTACTCAACCAAGGAACAAACCTCAGACTAAG
                                                                                                                                   | TGTCCCAGTGGAGGAGTCCCAGGGACCACGTGGACAATTCTTGGATACTGTCTTGGCA
                                                                                                                                             21 CysProSerGlyGlyGlnSerGlnGlyProArgGlyGlnPheLeuAspThrValLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell receptor beta chain ANA 11.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — SEQUENCE FROM N.A. MEGUENCE FROM N.A. MEGUENCE FROM N.A. MEDLINE=85242712; PubMed=2989826; Angiolillo A.L., Lamoyi E., Bernstein K.E., Mage R.G.; Identification of genes for the constant region of rabbit T-cell receptor beta chains." Proc. Natl. Acad. Sci. U.S.A. 82:4498-4502(1985).
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Submitted (APR-1987) to the PIR data bank
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187 rpTrpValAsnGlyLysGluValHisAsnGlyValSerThrAspProGlnProTyrLysG
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                                                                                                                                                                                                                                                                                                                                                                                          24 LeuThrMetThrProGluHisAlaArgProProThrThrThrAlaMetLeuTyrAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                          993 ---CTCTGGCATACCCCACATGCAAAGCACAAAGAACATTTATCCATACATCTCAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1110 GTGGGCAAGTATATTCTGCTCATCAATGGTCATTGGCTATGTACTTTGTGCAGGGAAGT
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| ::: b 116 GluGluLeuProProAlaProGlnArgGlnHisSerLeuProLeuHis-IleThrArgPr 135 | 3045 CTCGTTTGAATTAACACAGCAGTCAGTT | 3073GTCATTGCCATGACGACGTCTATCT | 3450 323 3493 3493 3522 3522 3562 366 3670 3702 400 400 400 419 |
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| Db 401 LeuLeuProAsnProProAlaAlaLeuProSerIleAlaTyrThrSerSerArgGly 419 | Qy 3765 AGG 3767 Qy Db 420 Lys 420 Db | PRESULT 4 VONC TYMAC TO 1-DEC-1992 (Rel. 24, Created) DT 01-DEC-1992 (Rel. 24, Last sequence update) DE 69 Map protein. OS TURING PROLOW mosaic virus (isolate TYMC). OY VONCILTA. TO VILUSE'S SERNA Dositive-strand viruses, no DNA stage; Tymoviridae; ON XCBL TAXID-31751; RN MEDLINE-92119261; PubMed=1731998; RT "Genomic RNA sequence of turing yellow mosaic virus isolate TYMC, a Cylladian of the State | 628 37 133 165 22 AGGCTGTGCCCTTC 2798 CTGGCTGTGCCCTTC 2798 |

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Pedersen O.
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     VARIANTS MODY3 HIS-12; GLN-131; GLN-205 AND CYS-263, AND VARIANT NIDDM
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MEDLINE=9100945; PubMed=8945470;

Yamagata K., Oda N., Kaisaki P.J., Menzel S., Furuta H.,

Vaxillaire M., Southam L., Cox R.D., Lathrop G.M., Boriraj V.V.,

Chen X., Cox N.J., Oda Y., Yano H., le Beau M.M., Yamada S.,

Nishigori H., Takeda J., Fajans S.S., Hattersley A.T., Iwasaki N.,

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"Mutarions in the hepatocyte nuclear factor-lalpha gene in maturity-

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           P20823; Q99861;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver-specific transcription factor LF-B1) (LFB1) (Transcription factor-1) (TCF-1).
                                                                                                                                                                                                                                                                                                                                                "More potent transcriptional activators or a transdominant inhibitor of the HNF1 homeoprotein family are generated by alternative RNA
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MEDLINE=97431550; PubMed=9287055;
Yamada S., Nishigori H., Onda H., Takahashi K., Kitano N.,
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                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a mutational hotspot in the MODY3 gene.";
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MEDLINE-97431548; PubMed-9287053;
Iwasaki N., Oda N., Ogata M., Hara M., Hinokio Y., Oda Y.,
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VARIANTS MODY3 ARG-107; TRP-131; MET-260 AND HIS-272.
  631 AA.
  PRT;
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                                                                                                                                                                                                                                                                                                                      MEDLINE=94038905; PubMed=7900999;
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                                                                                                                                                                                                                                                                                                                                                                            processing.";
EMBO J. 12:4229-4242(1993)
  STANDARD;
                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel mutations and
                                                                                                                                                                                                                                                                                                                                      I., Yaniv M.;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=9606;
                                                                                           ICF1 OR HNF1A.
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alpha gene in Japanese subjects with IDDM.";
Diabetes 46:1643-1647(1997).
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MEDLINE=97184312; PubMed=9032114;
Kaisaki P.J., Menzel S., Lindner T., Oda N., Rjasanowski I., Sahm J. Meincke G., Schulze J., Schmechel H., Petzold C., Ledermann H.M., Sachse G., Boriraj V.V., Menzel R., Kerner W., Turner R.C., Yamagata K., Bell G.I.;
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T., Bell G.I.,
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MEDLINE=97266232; PubMed=9112026;
Urhammer S.A., Rasmussen S.K., Kaisaki P.J., Oda N., Yamagata K
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Boriraj V.V., Chevre J.-C., Boccio V., Cox R.D., Lathrop G.M.,
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1134 AAAIGGICAIIGGCIAIGIACITIGIGCAGGAAGIACAIIAICIACAGICACAAAAAIG 1193
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                                                                                                                                                                                                                                                                                    GATCATCACACTCTTCTTCATCTGTTGCCATGCTGGAGCCCCACCAGGCAAGAGGGG 617
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407 SerLeuPro---GlyValMetThrIleGlyProGlyGluProAlaSerLeuGlyProThr
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GAGGAATAAATTACAAGTGGTCAAGGTTGCATCCTTTTGAGCTCAGGACCTGCTTGTAAG
                                 ----AsnArgAlaGluCysIle
                                                                                         243 GlnArgGlyValSer---ProSerGlnAlaGlnGlyLeuGlySerAsnLeuValThrGlu
                                                                                                                                        CAGCTCTATCTGGGACACCATCTTGACCAAACACCCAAGAAGGCATCTACAACACCATCTG
                                                                                                                                                                          ValArgValTyrAsnTrpPheAlaAsnArgArgLysGluGluAlaPheArgHisLysLeu
                                                                                                                                                                                                                                                                                                                        301 AlaHisSerSerPro---GlyLeuProProAlaLeuSerProSerLysValHisGly
                                                                   405 CCGAGAGGGITCTCTGGCCCTAATCTAGCCAAGCACCAIGGAGAAACAGTGCCTTCTT
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                            ||| ::: ||| GluThrLeuValGluGluCys
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                                                                                                                                                                                                         MEDLINE=98425814; PubMed=9754819;
Chevre J.-C., Hani E.H., Boutin P., Vaxillaire M., Blanche H.,
Chornet N., Pardini V.C., Timmit J., Larger E., Charpentier G.,
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other MODY genes.",
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Morikawa A., Inoue I., Takeda J.,

"Identification of mutations in the hepatocyte nuclear factor-lalpha gene in Japanese subjects with early-onset NIDDM and functional

plapetes 48:645-648(1999).
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                                                                                                                       an uncommon
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Takeuchi T., Takeda J.;
"Mutations in the hepatocyte nuclear factor-1 alpha gene 'MODY3'
mutations in the hepatocyte nuclear factor-1 alpha gene 'MODY3'
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                                                                                                              "Hepatocyte nuclear factor lalpha coding mutations are an uncomm contributor to early-onset type 2 diabetes in Ashkenazi Jews."; Diabetes 47:967-969(1998).
                                                                                                                                                                                         VARIANTS MODY3 ASP-31; TRP-159; THR-161; TRP-200 AND TRP-271.
                                                                                                                                                                                                                                                                                                                                                     VARIANTS IDDM LYS-48 AND GLY-241.
MEDLINE-99083111; PubMed=9867222;
Moeller A.M., Dalgaard L.T., Pociot F., Nerup J., Hansen T.,
                                                VARIANTS LEU-27; ASN-487 AND ARG-514.
MEDLINE=98265912; PubMed=9604876;
Behn P.S., Wasson J., Chayen S., Smolovitch I., Thomas J.D.,
Glaser B., Permutt M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98284534; PubMed-9621514;
Nishigori H., Yamada S., Kohama T., Utsugi T., Shimizu H.,
Takeuchi T., Takeda J.;
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                  Genet. 6:583-586(1997)
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31.55%
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| 247 251 | 2824 CCTGCACCAAACCCAGGGATGTGGAAGACATCTCCCCACAACTGCCAC 2871 ::: ::: ::: :: :: :: 252 ArgSerProSerProAlaVallleArgLysThrAlaGlylleLeuProHisProLysLeu 271 | 2872 TGCTCACCAGGACAAGCTGCCCTTCCTGTCTCCACCTCTCAGAATGGATGG | 2932 CTGGGGAGGGTGACGCTGACACGTAGTGTCAGATATGATCTAGGAGGCGG 2991 | 2992 ATCACCGGGATCCGGGACCATACAAGTAACATGGTTTCCATGGCAACTGCTTGC 3045 | 3046TGGTTTGAATTAAGAGGAGTCAGTTGTCATTGCCATGACAGGCCTCTA 3096 315 ValargSerAsnSerLeuGlnGlnThrProlleLeuMetGlyHisPheLysSerLeuGly 334 | 3097TCTCCAGGCACAATGTCCCTGCTGTCTCCTAATCCA | 3136 GACTTGCTCACCCCAGGGATGAAACACCCAGAAACTCACTTCTCAG 3183 | 3184TCACTTCCACAGCCGATGACTCAGAAGAGCCAAACCCAGAATGGGGCC 3231 | 3232 TCTCTTTCCCCATCACAGACTCCCCTGACAACCTTCCTGGCGTAACTAGAGGAGTCCC 3291 | 3292 AGTGCAGGATAGGCCCTAAACGTTTTGTTAAATAAACAGGGGCATGAAAGGAGC 3345 | 3346 CTAAGGCCATTGTTGATATCCACTCTCTTTCCACTTCCTTCTCATCTT 3396 :: | 432 Leu | 455 HisProdluGlualateuArg | | 3669 CAGGCTCCGGAGGCAGCCAGAGGAGGCCTTTCCCCATTGCTCCTTTCCCCATTGCTCAA 3728 | |
|-------------|---|--|--|---|---|--|--|--|--|--|--|--|---------------------------|------|---|------|
| 4 0 | & a | \$ 8 8 | & a | QY | δδ Op | Oy Op | S d | Qy Dp | δδ G | ò a | da oy | 4 8 8 8 | oy Oy | S a | \$ 8 8 | 8 |
| ::: ::: | Qy 1254 CCCCATACACCATCTATTCCATAAACCACTCAGGTTACAGATGCATGC | Qy 1314AACTCTACACATAAACTTTTACTGGAAGTACTCATAATTGGACATTCC 1361 ::: bb 575 IleGlnHisLeuGlnProAlaHisArgLeuSerAlaSerProThrValSerSerSerS 594 | Oy 1362 AGCAACCTGCTACAGTCC 1379 Db 595 LeuValLeuTyrGlnSer 600 | RESULT 6 V70K_OYMV ID V70K_OYMV STANDARD; PRT; 597 AA. AC P20130: | | OS Ononis Yellow mosaic virus. OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tymoviridae; OC Tymovirus. OX NCBI TaXID=12153; | | RT "Nucleotide sequence of the ononis yellow mosaic tymovirus genome."; RL Virology 172:555-563(1989). CC -1- FUNCTION: Not known. CC -1- SIMILARITY: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIBUSES | This | | CC | Length: Matches: Conservative: Mismatches: Indels: Gaps: | AAGCACTCAGGCCTC | 2701 | ProleuproserSeriuvsProleuserLeuGlalagivchorokverois | 2764 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: In fetal brain exclusively in pontine nuclei. SIMILARITY: BELONGS TO THE SAL FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                        SECURNCE FROM N.A. (ISOFORM 1).

MEDLINE-97131507; PubMed=8975705;

Kohlhare J., Schuh R., Dowe G., Kuehnlein R.P., Jaeckle H.,

Kohlhare J., Schuh R., Dowe G., Kuetzachmar H.A., Koehler A.,

Schroeder B., Schulz-Schaeffer W., Kretzachmar H.A., Koehler A.,

Mueller U., Raab-Vetter M., Burkhardt E., Engel W., Stick R.,

Mueller U., Raab-Vetterization, and organ-specific expression of two

novel human zinc finger genes related to the Drosophila gene spalt.",

Genomics 38:291-298(1996).
                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=9794994; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Nagase T., Ishikawa K., Kotani H., Nomura N., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note=No experimental confirmation available;
TISSUE SPECIFICITY: Highest levels in adult brain (in different
areas). Lower levels in heart; very low levels in kidney and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 602219; -. Ginucleus; NAS. GO:0005634; C:nucleus; NAS. GO; GO:0005700; F:transcription factor activity; NAS. GO: 00:0006375; P:regulation of transcription, DNA-dependent; NAS. InterPro; IPR007087; Znf_C2H2.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 7 C2H2-type zinc fingers.
                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 541-1005 FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 11-1007 FROM N.A. (ISOFORM 2).
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EMBL; AB002358; BAA2<u>1</u>638.1; ALT_INIT.
EMBL; AF465630; AAL74188.1; -.
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        507 TrpValGlnCys 510
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                                                SAL2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CysAlalysValPhedlySerAspSerAla---LeuGln11eHi 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAAGCTGGCCATTTTGCTGCTGTGTGGGGGGGTGCTGTCAGTGGCATGCCC--- 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----------AAACCCAAAGCTGGAAGAGAATAAATTACAAGTGGTCA 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: ||| ::: ||| 391 sLeuArgSerHisThrGlyGluArgProTyrLy8CysAsnValCysGlyAsnArgPheTh
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                                                                                                                                              protein; Zinc-finger;
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POLY-PRO.
QLISDCEGPSASEN -> SRLGVPCGEPAELG (in
DR Pfam; PF00096; zf-C2H2; 7.

DR ROASITE; 8M00355; ZnR C2H2 1; 7.

DR PROSITE; PS00028; ZINC FINGER C2H2 2; 7.

DR PROSITE; PS50157; ZINC FINGER C2H2 2; 7.

DR PROSITE; PS50157; ZINC FINGER C2H2 2; 7.

DR PROSITE; PS50157; ZINC FINGER C2H2 2; 7.

KW Mctal-binding; Repeat; Alternative splicing; Polymorphism.

FT ZN FING 401 423 C2H2-TYPE 1.

FT ZN FING 691 653 C2H2-TYPE 3.

FT ZN FING 691 713 C2H2-TYPE 4.

FT ZN FING 691 713 C2H2-TYPE 5.

FT ZN FING 691 713 C2H2-TYPE 6.

FT ZN FING 940 940 960 POLY-GLY.

- ZN FING 940 POLY-GLY.

- ZN FING 940 POLY-GLY.

- SRLG!

- - SRLG!
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V -> M (IN REF. 1).
FPYVLEP -> LPLCARA (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VAR 014129.
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R -> G (in dbSNP:1263810)
/FTId=VAR_014131.
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449 yLeuProTyrGlyMetSerValProProGluLysAlaGluGluGluAlaAlaThrProGl 469
                           ------TGAAGAAGACCTCTGGATCTCTGCTCAACCCAAGCTTCTCCAGATGGAGA 709
                                                          ----AlaTh 487
                                                                                                                                     770 AGCCTCCTTCTGACCACACACACATTTCAGGAACCCCTGAAATAATGCACTATGTCCA 829
                                                                                                                                                                  ------diyLeuProAlaPheAsnLysPheValLe 513
                                                                                                                                                                                            830 TGTCCACAGAGTAACTACTCAACCAAGGAACAAACCTCAGACTAAGTGTCCCAGTGGAGG 889
                                                                                                                                                                                                                     513 uMetLysAlaVal-----GluProLysAsnLysAlaAspGluAsnThrProProGlySe 531
                                                                                                                                                                                                                                                  GCAGTCCCAGGGACCACGTGGACAATTCTTGGATACTGTCTTGGCAGCTATGTGTCCAAT 949
                                                                                                                                                                                                                                                                          531 rGluGlySerAlaIleSerGly---ValAlaGluSerSerThrAlaThrArgMetGlnLe 550
                                                                                                                                                                                                                                                                                                                                  550 uSerLysLeuValThrSer-----LeuProSerTrpAlaLeuLeuThrAsn-HisP 567
                                                                               710 AGAGACCATCACTGCCTGTTTAGTTAGGCAGGAAGCAGAGGTGTTTCCTTTCTGGGGCTA
                                                                                                  |||::::::|||
487 rGlüSerLeuThrLeuLeuSerThrSerAlaGlyThrAlaThrAlaPro------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=89386006; PubMed=2506527;

Kawamura S.,

Kawamura S.,

KNucleotide sequence of the gorilla immunoglobulin alpha 1 gene.";

Nucleic Acids Res. 17:6732-6732 (1989).

-! FUNCTION: Ig alpha is the major immunoglobulin class in body

secretions. It may serve both to defend against local infection
and to prevent access of foreign antigens to the general

immunologic system.

-! SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                    469 yGlyGlyValGluArgLysProLeuValAlaSerThrThrAlaLeuSer--
                                                                                                                                                                                                                                                                                                                                                               1010 TGCAAAGCACAAAGAACATT---TATCCATACATC 1041
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heLysSerThrGlySerPheProPheProTyrVal 578
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10-FEB-1991 (Rel. 17, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1g alpha-1 chain C region.
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HSSP, P01810, 2FBJ.
INTEPPO: IPR00710, Ig-like.
InterPro: IPR00359; Ig_c1.
InterPro: IPR00306; Ig_MHC.
Ffam, PF0047; Ig1, 2.
PROSITE; PS50835, IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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27 LeuValGln-----GlyPhePheProGlnGluProLeuSerValThrTrpSerGlu
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                                                                                                                                                                     OR 123-182 (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH HEAVY CHAIN) (OR 180).
INTERCHAIN (WITH HEAVY CHAIN OF ANOTHER SUBUNIT) (BY SIMILARITY).
 Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GlnAspValThrValProCysArgValProSerThrProProThr-----
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N-LINKED (GLCNAC. .) (POTENTIAL).
4820E8DB02AC7514 CRC64;
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IG-LIKE 2.
IG-LIKE 3.
INTERGHAIN (WITH LIGHT CHAIN)
SIMILARITY).
                                                                                                                                         INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                    BY SIMILARITY.
INTERCHAIN (WITH J CHAIN) (BY
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161
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Matches:
Conservative:
Mismatches:
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                 37755 MW;
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108.00
28.37%
21.49%
1.35%
Immunoglobulin domain;
NON TER 1 1
DOMAIN 6 98
DOMAIN 125 220
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.
Transcription regulation; DNA-binding; Zinc-fing
Nuclear protein; Repeat.
                                               C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5.
C2H2-TYPE 6.
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18.27%
1.35%
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                                    Nuclear protein; R
ZN FING 237
ZN FING 453
ZN FING 569
ZN FING 758
ZN FING 758
ZN FING 605
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                                                                                                                                                                                                                                                                                                                   1515 CTCATTGCCACTGAGAGGTGTTTAATGTGATCCA-----AGACCTCTCTGTGA 1562
                                                                                                                                                                                                               TIGATACAGACACCAAGITICIGIGCCICIGACCCCICGCCCAGGAGAIGITIAA 1454
                                                                                                                                                                                                                                                                1455 AGTGTGATGGTTCAAAATTCATTGAAAGCTCTTTTCTTGTAACTCATGACAAGTCCGTC 1514
                                                      290 ACAGATGCATGCTTTCCTATTCTAACTCTAAACTTTTACTGGAAGTACTCATA 1349
  1230 ATACAATTICCIAACCAGCAAGGCCCCCATACACCATCTATTCCATAAACCACTCAGGTT 1289
                                                                                                                                                                                                                               211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Tanaka A., Kotani H., Nomura N., Ohara O.; Tanaka A., Kotani H., Nomura N., Ohara O.; Tanaka A., Kotani H., Ioomura Sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:197-208 (1999).

-!- FUNCTION: May function as a transcription factor.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                -----CyscysHisPro---ArgLeuSerLeuHisArgProAlaLeuGluAspLeuLeu
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                     SIMILARITY: Contains 6 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=99397452; PubMed=10470851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P15822; 3ZNF.
Genew; HGNC;220042; ZNF409.
InterPro; IPR007087; Znf CZH2.
Fam; PF00096; zf -C2H2; 5.
SMART; SM00355; ZnF_CZH2; 6.
                                                                                                               1350 ATTGGACATTCCAGCAACCTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB028979; BAA83008.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc finger protein 409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZNF409 OR KIAA1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z409 HUMAN
                                                                                       122
                                                                                                                                                                                                                    1395
                                    110
                                                                                                                                         139
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---ProSerAspProProGlnProTy 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 eprogluglyglnglugluAspGlyGlyLeuĊyaProProleuAsnGlnSerSerProTh 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTAGCCAAGCACCATGGAGAATCAGTGCCTTCTTCAGCTCTATCTGGGACACCATCT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ThrLeuProAlaProValGlySerProGl 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GCTTGTAAGCCGAGAGGGTTCTCTGGCCCTAA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::::::||||||
-SerAspIleProLeuAspAsnSerSerThrValAsnMetGluAlaAsnValAlaGlnTh 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AAGCTGGA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    talaLeuSerProProSerProProThrAlaThrTrpAspProSerProThrGlnAlaLy 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 LeuThr---ProAlaGlnTyrGlnGlyLeuSerGlySerProAlaValLeuGlnGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 dlyprometdlyasnSerGlyGlyAsnHisValAlaValPheTrpLeuCysLeuLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: | | | | :::::: | | | 243 ArgLeuGlyPheSerLysProGlnAlaPheMetAspHisThrGlnSerHisGlyValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGACCTTCCCAAGGACACACACTGAACTGGGCGGTGATCAGGATCTGAATGCACAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GGGTGTTCAGCGATTGTTTACTACGTTGAACGTGACCTCCAGGAAAGCAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GGCTCCCCA----AGCTGGCTGGCCATTTTGCTGCTGTGTGTGGCTGCT
finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGGAATAAATTACAAGTGGTCAAGGTTGCATCCTTTTGAGCTCAGGACCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GGCCGAGATCCCCTGACAACGCAAAGCAAGAAGTAACGTGGAAGGA--
                                                                                                                                                                       PRO-RICH.
EBGBFF9A0B939217 CRC64;
                                                                                                                                                                                                                                                       862
97
53
158
223
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCTGCAGGAAGCCCTTCCGCGGACCGAAAGATTGTT----
                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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sapiens (Human)

| 431 | 72 | | ACA 787 | 434 | IAC 847 | 445 | ACC 904 | 457 | FAC 964 | 457 | AGA 1024 | ::: nGl 466 | AC 1084 | 3Pr 477 | 1109 | IAr 497 | CT 1126 | Th 517 | AC 1186 | G1 537 | CA 1246 | Se 557 | CC 1306 | Ту 576 | AA 1366 | As 596 | | (i |
|--------------|--|-----|---|------|----------------------------|--|----------------------|-----|--|-----|---|----------------|--|----------------------------------|------|--|---------|--------|---------|--|--|---|--|---|--|--------|----------------------|---|
| AlaProAlaAla | ACCTCTGGATCTCTGCTCAACCCAAGCTTCTCCAGATGGAGAAGAGACCATCACTGCCTG | | TTTAGTTAGGCAGGAAGCAGAGGTGTTTCCTTTTCTGGGGCTAAGCCTCCTTCTGACCACA | | CACAGACATTTCAGGAACCCCTGAAA | ::: -LeuSerLeuSerSerHisMetSerLeuLeuHis | TCAACCAAGGAACAAACCTC | | ACGTGGACAATTCTTGGATACTGTCTTGGCAGCTATGTGTCCAATAGCAATGCTCCTTAC | | TGCAGACCCAGGCATGCCTCCCACTGTCTCTGGCATACCCCACATGCAAAGCACAAAGA | | ACATITATCCATACATCTCAATATGGTTCCCAAGTGTGTGCACATGCACGTAACACACAC | nThrLeuAspValHisMetGlnGluLysHis) | | oGluSerAsnSerHisCysSerTyrCysSerAlaGlyGlyAlaHisProArgLeuAlaAr | | | | rThrThrLysGlyAsnLeuSerlleHisMetGlnSerAspLysHisLeuAlaAsnLeuGl | AAAAATGTCTCATGGGAAAGCCTTGCCAGATTCAGACACATATATACAATTTCCTAACCA | nGlyPheGlnAlaGlyProGlyGlyGlnGlySerProThrGluAlaSerLeuProProS | GCAAAGGCCCCCATACACCATCTATTCCATAAACCACTCAGGTTACAGATGCATGC | rAladlyAspLysGluProLysThrLysSerSerTrpGlnCysLysValCysSerTy | TATTICTAACTCTACACATAAACTITTACTGGAAGTACTCATAATIGGACATTCCAGAAA | Σ. | CIGGLACAGTCCCCACCTTG | STANDARD; STANDARD; PRT; 2063 AA 29; Q9UH74; Q9UR86; (Rel. 41, Last sequence update) (Rel. 43, Last annotation updat ptor coactivator 6 (Amplified if ified transcriptional coactivation eracting protein, 250 k RAP250) (NRC RAP250) (Thyroid h 3 OR RAP250 OR TRBP OR KIAA0181 |
| 428 | 899 | 431 | 728 | 432 | 788 | 435 | 848 | 446 | 908 | 457 | 965 | 458 | 1025 | 466 | 1085 | 477 | 1110 | 497 | 1127 | 517 | 1187 | 537 | 1247 | 557 | 1307 | 9 10 0 | 1367 | HHZQQQUHZ O WHO O WZ |
| d | ò | QQ | à | qq | ò | qq | δ | QQ | ò | Ωp | δ | ΩD | ò | q | à | QQ | δλ | qq | δλ | qq | ò | Dp | ογ | qq | ð 5 | 3 8 | r F | RESULT NGO6 HIT NGO6 |

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REDICINGE FROM N.A.

REDICINE—21639749; PubMed=11780052;

RA BEDICINE—21639749; PubMed=11780052;

RA Deloukas R., Matchews L.H., Ashurst J., Bubbage A.K., Bagguley C.L.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clae C.M.,

RA Chapman J.C., Collier R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Barfham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Huckle E., Hunt S.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt S.L., McConnachie L.J., McChurray A.A.,

RA Jehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McChurray A.A.,

RA Millimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Mahajan M.A., Samuels H.H.; "A new family of nuclear receptor coregulators that integrates nuclear receptor signaling through CBP.";
                                                                                                                                                                                                                                                                           nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND INTERACTION WITH PPARA; PPARG; ESR1; ESR2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gustafsson J.-A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ko L., Cardona G.R., Chin W.W.;
"Thyroid hormone receptor-binding protein, an LXXLL motif-containing
protein, functions as a general coactivator.";
Proc. Natl. Acad. Sci. U.S.A. 97:6212-6217(2000).
                                                                                                     REQUENCE FROM N.A., AND INTERACTION WITH CREBEP, NCOA1, GTF2A, TBP, RXRA, ESRI, RARA AND THRA.

MEDLINE=20036574; PubMed=1056749.

Lee S.-K., Anzick S.L., Choi J.-E., Bubendorf L., Guan X.-Y., Jung Y.-K., Kallioniemi O.P., Kononen J., Trent J.M., Azorsa D., Jung Y.-K., Kallioniemi O.P., Kononen J., Trent G.M., Azorsa D., Anuclear factor ASC-2, as a cancer-amplified transcriptional coactivator essential for ligand-dependent transactivation by nucle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          У.
by
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., HOMODIMERIZATION, AND INTERACTION WITH CREBEP;
RXRA; ESR1; NR3C1; RARA; VDR AND THRA.
MEDLINE=20325329; PubMed=10866662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., PHOSPHORYLATION BY PRKDC, AND INTERACTION WITH THR; RAR; EP300 AND CRSP3.
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIANE=96281124; PubMed=8724849; Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDMA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20148724; PubMed=10681503;
Caira F., Antonson P., Pelto-Huikko M., Treuter E., Gustafss
"Cloning and characterization of RAP250, a nuclear receptor
                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 274:34283-34293(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell. Biol. 20:5048-5063(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coactivator.";
J. Biol. Chem. 275:5308-5317(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20283976; PubMed=10823961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lymphocytes;
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TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                            receptors in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
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The Transmission of the LXXLL motif of coactivator TRBP defines

RT "Ser-884 add accent to the LXXLL motif of coactivator TRBP defines

RT "Ser-884 and TR8.";

RUSTION: Nuclear receptor coactivator that directly binds nuclear

receptors and stimulates the transcriptional activities in a

normone-dependent fashion. Coactivates expression in an agonist-

and AR2-dependent manner. Involved in the coactivation of

different nuclear receptors, such as for steroids (GR and ERS),

different nuclear theorems of the receptor coactivator. May

retinoids (RARS and RXRS), thyroid hormone (TRS), vitamin D3 (VDR)

cactivator, rather than just a nuclear receptor coactivator. May

also be involved in the coactivation of the NF-kappa-B pathway.

MAY coactivate expression via a remodeling of chromatin and its

interaction with histone acetyltransferase proteins.

cactyltransferase RP300 and CRBBP, and the basal transcription

function. Interacts with NCOA1, CRSP3, RBM14, the histone

acetyltransferases RP300 and CRBBP, and with the

methyltransferases RP300 and CRBBP, and with the

methyltransferases NCOA6IP and HRW111/PRWT2. Belongs to the

retinoblastoma-binding protein NRP0-3 (RBPS, alpha-and beta-

retinoblastoma-and manner NRP0-3 (RBPS, alpha-and beta-

retinoblastoma-and nrown nrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cervical carcinoma;

MEDLINE=22371496; PubMed=12482968;

GOO Y.-H., Sohn Y.C., Kim D.-H., Kim S.-W., Kang M.-J., Jung D.-J.,
Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,
Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee Y.C.,
Lee J.W.;
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A. Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21423955; PubMed=11443112; Iwasaki T., Chin W.W., Ko L.; Iwasaki T., Chin W.W., Ko L.; Ilandilloation and characterization of RRM-containing coactivator activator (CoAA) as TRBP-interacting protein, and its splice variant as a coactivator modulator (CoAM).";
                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
                                                                                                                                                                                                                                                            MEDIINE=21417756; PubMed=11517327;
Zhu Y.-J., Qi C., Cao W.-Q., Yeldandi A.V., Rao M.S., Reddy J.K.;
Zhu Y.-J., Qi C., Cao W.-Q., Yeldandi A.V., Rao M.S., Reddy J.K.;
"Cloning and characterization of PIMT, a protein with a
methyltransferase domain, which interacts with and enhances nuclear
receptor coactivator PRIP function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methyltransferases NCOAGIP and HRWTiL1/PRWT2. Belongs to the ASC-2/NCOA6 complex (ASCOM), which contains ASC-2/NCOA6, the retinoblastoma-binding protein RBQ-3/ RBBP5, alpha- and betatubulins, the trithorax group proteins MLL2 and MLL3, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel steady-state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activating signal cointegrator 2 belongs to a novel steady-st
complex that contains a subset of trithorax group proteins.";
Mol. Cell. Biol. 23:140-149(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ko L., Cardona G.R., Iwasaki T., Bramlett K.S., Burris T.P.,
Chin W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH HRWILLI.
MEDLINE=22151129, PubMed=12039952;
Qi C., Chang J., Zhu Y., Yeldandi A.V., Rao S.M., Zhu Y.-J.
Identification of protein arginine methyltransferase 2 as coactivator for estrogen receptor alpha.";
J. Biol. Chem. 277:28624-28630(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS OF 883-THR--GLU-894, AND PHOSPHORYLATION.
MEDLINE-21635582; PubMed=11773444;
                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 98:10380-10385 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH MLL3 AND THE ASCOM COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 276:33375-33383(2001)
                                                                                                                                                                                                                                                INTERACTION WITH NCOASIP
                                                                                                                                             Rogers
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TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain, prostate, testis and ovary; weakly expressed in lung, thymus and

SUBCELLULAR LOCATION: Nuclear.

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2865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2917 CCCIAGAAIGGAIGGCIGGGGAGAGGIGGAGGCIGACAGCIGAGACGIAGIGICAGAIAI 2976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1043 prolysservalArgLeuProValSerGlnAsnValHisProProArgGlyProLeuAsn 1062
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTITGACCAGAGA-----AAGAAGCACICIGGIICICIAICCCCTIGICACAIAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProAspSerdinArgMetProMetGlnGlnSerGlySerVal---ProValMetVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTTGTCATGGGGCCTCTGGCTGTGCCCTTCACATAACAGAATAACTTGCCATCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerieuGlnGlyProAlaSerValProProSerProAspLysGlnArgMetProMetPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GGGATGTGGAAGACATCTCCCCACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2866 IGCCACTGCTCACCA-----GGACAAGCTGCCCTTCCT---GTCTCCACTCTCAGTCC
 -!- DOMAIN: Contains two Leu-Xaa-Xaa-Leu-Leu (LXXLL) motifs. Only motif 1 is essential for the association with nuclear receptors, while adjacent Ser-884 displays selectivity for nuclear receptors.-!- PTM: Phosphorylated by PRKDC.-!- PTM: Phosphorylation on Ser-884 leads to a strong decrease in binding to ESR1 and ESR2.
-!- MISCELLANEOUS: Frequently amplified or ovexpressed in colon,
                                                                                                                                           !- CAUTION: Ref.1 (AAR16403) sequence differs from that shown due
a frameshift in position 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:00049966; Fithyroid hormone receptor binding; IDA.
GO:0003713; Fitzanscription co-activator activity; IDA.
GO:0001720; Fitzanscriptional activator activity; IDA.
GO:0001720; Pibrain development; ISS.
GO:0001701; P:embryonic development (sensu Mammalia); ISS.
GO:0001707; P:heart development; ISS.
GO:003099; P:myeloid blood cell differentiation; IDA.
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97
47
130
141
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005634; C:nucleus; IDA.
GO:0005667; C:transcription factor complex; TAS.
GO:0003682; F:chromatin binding; ISS.
GO:0030331; F:estrogen receptor binding; TAS.
GO:0046965; F:retinoid X receptor binding; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-776-827-10 (1-4460) x NCO6_HUMAN (1-2063)
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                                                                                                                                                                                                                                                                                                                                            EMBL, AF177388; AAF13595.1; -...
EMBL, AF208227; AAF16403.1; ALT_FRAME.
EMBL, AF245115; AAF78400.1; -...
EMBL, AR171667; AAF78003.1; -...
EMBL, D80003; BAA11982.1; -...
EMBL, BA0003; BAA11982.1; -...
EMBL, BANC:15936; NCOA6.
                                                                                                                                         breast and lung cancers.
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| Tymov | NO [1] TAX | RX MEDLINE= RA Keese P. | · | | | C This SWI | | modif | | | | SEQUENCE | Alignment Sco Pred. No.: | Score: Percent Simil | Best Local Sir Query Match: | DB: | US-10-776-827 | Qy 2748 | Db 40 | Qy 2799 | Db 60 | у 2859 | DP 40 | y 2916 | b 92 | y 2976 | 56 q | y 3036 | 0 103 | 4 3058 | 5 123 | 3114 | 143 | ~) | | 3231 |
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| _ | | | | | | | | | | | | | | | m O | | | | Δ | о — | Δ | <i>δ</i> | | <i>&</i> | qu | δ | qa | δ | ପ୍ | λō | વ ਹ | δ | ପ୍ | <i>λ</i> δ | <u>ବ</u> - | - O |
| Db 1141 Pro | Qy 2977 GATCTAGGAGGGGGATCACCGGGATCCGGGACCATACAAGTAACATGGTTTCCATGGA 1036 | | Qy 3037 ACTGCTTGCTCGTTTGAATTAAGACAGCAGTCAGTTGTCATTGCCATGACAAGGCCTCTA 3096 | Db 1155 ValLeuProGlnAsnGlnLeuMetMetThrGlyPro 1166 | QY 3097 TCTCCAGGCACAATGTCCCTGCTGTCCTAATCCAATGGACTTGCTCTCACCCCAGGGA 3156 | | Qy 3157 TGAAACACCCAGAAACTCACTTCTCAGTCACTTCCACAG3195 | | Qy 3196CCGATGACTCAGAAGACCAAAACGAGAATGGGGCTCTTTTC 3240 | Db 1199 AsnValAlaAlaProThrGlnThrSerArgProLy8ThrProAsnArgAlaSerProArg 1218 | 3241 | 1219 | 3298 | Db 1238 erLeuSerProGluArg 1243 | Qy 3358 TIGATAICCACICTCTTTTCCACTTCCTTCTTTTTTTTCGAIGTTTTAIGCTTC 3417 | | QY 3418 TCTGATTCCTCTTCTGCCTGCACCAGCCCCAGCCCTTTATTCCTCTCCATTTT- 3476 | Æ | | | Qy 3508 ACTGGCAACCCATGGGACCTCAGGACCAGAGACTGCTTGACT 3549 | ::: ::: | Qy 3550 CATCTGGGGAGGTAAGTTCACGGGGGGAAAAAAAAAAGATCCTAAAGAAGAGGCTTCCT 3609 | Db 1311 snSerGlyLysGlnSerAenSerGlyAlaThrLysArgAlaSerProSerAenSerArgA 1331 | QY 3610 AGACCAGGACAGGGTCCAGAAAGACATCCCCTAGGACTTCTGAGCAGCTTTA 3666 | Db 1331 rgSerSerProGlySerSerArgLysThrThrProSerProGlyArgGlnAsnS 1349 | 1 | | QY 3693AGGCCTTTCCCCATTGCTCCTTTCCCCATTGCT 3725 | 138 | RESULT 11 | 7.0% IIMVA D V70K IYMVA STANDARD; PRT; 628 AA. | 7. | | S Turnip yellow mosaic virus (Australian isolate). C Viruses; seRNA positive-strand viruses no num etane. | |
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nArgGlnHisSerLeuProLeuHisIleThrArgProSerArgPheProHisHisPheHi 143
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P., Mackenzie A., Gibbs A.;
Putide sequence of the genome of an Australian isolate of turnip
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WCTION: Not known.
MILARITY: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES.
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F03251; Tymo 45kd 70kd; 1.
E 628 AA; 68740 MW; 67CD342A09161D96 CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                CTICIGCCTGCACCAGCCCCAGCCCTTTATTCCTCTCCATTTT-----
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sal-like protein 2 (Spalt-like protein 2) (MSal-2)
SALL2 OR SAL2
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Q9QX96;
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pSerAlaLeuGlnIleHisLeuArgSerHisThrGlyGluArgProTyrLysCysAsnVa 404
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          throughout embryonic development.
        TISSUE SPECIFICITY: Expressed throughout embryonic development adult predominantly in brain.
SIMILARITY: BELONGS TO THE SAL FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CTTCTTCAGCTCTATCTGGGACACCATCTTGACCAAAAACACCAAAGAAGG-
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Matches:
Conservative:
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(Probable)
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C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5.
C2H2-TYPE 6.
C2H2-TYPE 7.
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POLY-PRO.
POLY-SER.
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| | 587 ATTGCTGCTGGAGCCCACCAGGCAAGAGGGCCCAGCCAGC | AGAAGAAGAAGGATGAAGACCTCTGGATCTCTCTGGATCTCTCTGGTCTCT | | 686 AACCCAAGCTTCTCCAGATGGAGAGAGACCATCACTGCCTGTTTAGTTAG | 480 rThrAlaLeuSerAlaThrGluSerLeuThrLeuLeuSerThrGlyThrSerTh 498 | | | 806 CCCTGAAATAATGGACTATGTCCATGTCCACAGAGTAACTACTCAACCAAGGAACAAACC 865 504 UProThrPheAsnivsPheValleumertssalaval | CCACGTGGACAATTCTTGGATAC | aAspGluAsnThrProProGlySerGluGlySerAlaIleAlaGlyValAlaAspSe | TGTCTTGGCAGCTATGTGTCCAATAGCAATGCTCCTTACTGCAGACCCAGGCATGCCTCC | : rGlySerAlaThrArgMetGlnLeuSerLysLeuValThrSerLeuProSe | | | | :: 7 alLeuGluProLeuGlyAlaSerProSerGluThrSerLysLeuGlnGlnLeuValGluL 597 | | ::: ::: 7 yslleAspArgGlnGlyAlaValAlaValAlaSerThrAlaSerGlyAlaProThrThrS 617 | | erAlaProAlaPr | | alLeuSerCysProArgAlaLeuArgLeuHisTyrGlyGlnHisGlyGlyGluArgProP 657 | 9AAATGTCTCATGGGAAAGCCTTGCCAGATTCAGA 1222 | | | | | | AN CHANDADD. DDM. OAA2 22 |
| | | | | | | | | | | 522 | 926 | 541 | 986 | 558 | 1046 | 577 | 1093 | 597 | 1123 | 617 | 1169 | 637 | 1189 | 657 | 1223 | 674 | 1261 | 694 | RESULT 13 APC HUMAN ID APC HIMAN |
| qa | å a | ò | qq | ò | qq | δŏ | <u>අ</u> | රි සි | ò | g | ò | qq | δ | q | δ | đ | δ | Д | ò | g | ò | q | ò | qq | δ | Q | ò | qq | AP TD |

APC HUMAN STANDARD; PRT; 2843 AA. P25054; Ol5162; Ol15163; Ol15163; Ol-MAY-1992 (Rel. 22, Last sequence update) Ol-MAY-1992 (Rel. 22, Last sequence update) Adenomate polyposis coli protein (APC protein).

Homo sapiens (Human)

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MEDLINE=20384842; PubMed=10926498;
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                                                                                   MEDLINE=91335210; PubMed=1651562;
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     Euteleostomi;
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Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                        MEDLINE=91330307; PubMed=1678319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95174843; PubMed=7661930;
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ЕМВО J. 20:6203-6212(2001).
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                    Eutheria;
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                                                                  SEQUENCE FROM N.A.
                                  NCBI_TaxID=9606;
                    Mammalia;
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Stella A., Montera M., Resta N., Marchese C., Susca F., Gentile M.,
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SER-2502.
  CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 2034-2049 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                            VARIANTS FAP.

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MEDLINE-95134544; PubMed-7833149;
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MEDLINE=91335211; PubMed=1651563;
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                                                                               interaction.";
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                                                                                                                       REVIEW ON VARIANTS.
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2281 GlüleüSerProValAlaArgGlnThrSerGlnIleĠİyĠİySerSerLysAlaProSer 2300
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                                                                                                                                                                                                                                                                                VARIANTS COLORECTAL CARCINOMA THR-880; ILE-890 AND VAL-1508.
MEDLINE=98080146; PubMed=9419979;
Miyaki M., Nishio J., Konishi M., Kikuchi-Yanoshita R., Tanaka K.,
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MEDLINE=98333712; PubMed=9724771;

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MEDLINE=98400248; PubMed=9731522;
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                                 GAATTAAGACAGCAGTCAGTTGTCATTGCCATGACAAGGCCT
                2301 ArgSerGlySerArgAspSerThrProSerArgProAla-
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01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
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-----ThrSerSerProLeuThrGluSerThrThrLeu-----LeuSerThr 4240
2944 GGAGGCTGACAGCTGAGGTAGTGTCAGATATGATCTAGGAGGGGGGGATCACCGGGATC 3003
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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P1C4_MOUSE STANDARD; PRT; 1964 AA.
P1695; 035442; 088314; 088316; Q62389; Q62390; Q9RIW9; Q9RIXO; 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Neurogenic locus notch homolog protein 4 precursor (Notch 4)
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Robbins J., Blondel B.J., Gallahan D., Callahan R.;
"Mouse mammary tumor gene int-3: a member of the notch transforms mammary epithelial cells.";
J. Virol. 66:2594-2599(1992).
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             MEDILINE=21374376; PubMed=11459441;

MEDILINE=21374376; PubMed=11459441;

MIZUTANI T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

"Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";

"Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";

"Droc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

"Jaggedl, Jaggedz and Daltal to regulate coll-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and appoptive programs (By similarity). May regulate branching morphogenesis in the developing vascular system.

"C -I SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1436-1600 FROM N.A.
MEDLINE=99252212; PubMed=10233982;
Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
Lintracisternal type A particle-mediated activation of the Notch4/int3
gene in a mouse mammary tunnor; generation of truncated Notch4/int3
J. Virol. 73:5166-5171(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryonic development from 9.0 dpc.
PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following
                                                                                                                                   TISSUE-Lung, and Testis;
MEDLINE-96281668; PubMed-8681805;
Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
Notch4/int-3, a mammary proto-oncogene, is an endothelial
cell-specific mammalian Notch gene.";
Development 122:2251-2259(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and testis.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,
"Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uyttendaele H., Ho J., Rossant J., Kitajewski J.;
"Vascular patterning defects associated with expression of activated
Notch4 in embryonic endothelium.";
Gallahan D., Callahan R.;
"The mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
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                                                                                                              SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 DISEASE: Loss of the extracellular domain causes constitutive activation of the Notch protein, which leads to hyperproliferation of glandular epithelial tissues and development of mammary
                                                   called
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.
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ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment call notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
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NOTCH EXTRACELLULAR TRUNCATION.
NOTCH INTRACELLULAR DOMAIN.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                carcinomas.
--- SIMILARITY: Belongs to the NOTCH family.
--- SIMILARITY: Contains 29 EGF-like domains.
--- SIMILARITY: Contains 3 Lin/Notch repeats.
--- SIMILARITY: Contains 5 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M80456; AAB38377.1; -...
EMBL; U43691; AAC526310.1; -...
EMBL; U43691; AAC52631.1; -...
EMBL; AF030001; AAB82004.1; -...
EMBL; AB016771; BAA32281.1; ALT_SEQ.
EMBL; AB016772; BAA32281.1; ALT_SINTT.
EMBL; AB016773; BAA32284.1; ALT_INIT.
EMBL; AB016774; BAA32285.1; -...
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PIR; A38072; TVWATS.

RISP, P08709; IDF9.

RGS, PG1:107471; Notch4.

InterPro; IPR002110; ANK.

InterPro; IPR002110; ANK.

InterPro; IPR001438; EGF Ca.

InterPro; IPR001438; EGF Ca.

InterPro; IPR002049; Laminin EGF.

InterPro; IPR0080829; Notch.

InterPro; IPR0080829; Notch.

InterPro; IPR0080829; Notch.

InterPro; IPR0080829; Notch.

Pfam; PF00008; EGF, Z7.

Pfam; PF00008; EGF, Z7.

Pfam; PF00008; EGF, Z7.

PRMYS; PR00010; EGFBLOOD.

PRINTS; PR00119; EGFLAMININ.

PRINTS; PR00119; EGFLAMININ.

PRNATT; SM002148; ANK, 6.

SMART; SM002149; ANK, FEP REGION; 1.

PROSITE; PS000829; ANK REPEAT; 5.

PROSITE; PS00082; EGF Z4; 11.

PROSITE; PS00187; EGF Z4; 21.

PROSITE; PS01186; EGF Z; 21.

PROSITE; PS01187; EGF Z4; 27.

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                                                                                                                                                                                          from the membrane. PTM: Phosphorylated.
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| COMPANY 115 112 EGF-LIKE 1. CALCIUM-ENNING (POTENTIAL) DOWNERS 115 112 EGF-LIKE 3. CALCIUM-ENNING (POTENTIAL) DOWNERS 115 112 EGF-LIKE 3. CALCIUM-ENNING (POTENTIAL) DOWNERS 115 112 112 EGF-LIKE 3. CALCIUM-ENNING (POTENTIAL) DOWNERS 115 112 | 1609 TTGCTTGGAGAAAGGCACTTTGCTGAGTGTTTGCGGGGTAATGTTTCACAGAGGGCT 1509 TTGCTTGGAGAAAGGCACTTTGCTGAGTGTTTGCGGGGTAATGTTTCACAGAGGGCT 1550 1619 | 1366 TIGCTGGAATGTCCAATTATGAGTACTTCCAGTAAAAGTTATGTGTAGAGTTAGAA 1310 | 1008 AspÀrġProCysHisProSerGlyThrAlaAlaCysHisSerLeuAlaAsnAlaPhelYr 102/ 1087 TGTGTGTGTTACGTGCACACTTGGGAACCATTGGATGT |
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| 661 CAT 626 | | ::: | 595 AGCAGCAATGGCAACAGATGAAGAGGTGTGATGATCACCAAGAGTGGCAGGACGAGGA 536 | 1178 GlyGlyAspGlyThrCysAspAlaGlyCysSerGlyProGly 1191 | 535 GGACTCCCAGGCAGATGGTGTTGTAGATGCCTTCTTGGTGTTTTGGTCAAGATGG 482 | 1192GlyAspTrpAspGlyGlyAspCysSerLeuGlyValProAspProTrpLys 1208 | 481TGTCCCAGATAGAGCTGAAGAAGGCACTGATTCTCTCCATGGTGGTGGTTAGATTA 425 | 1209 GlyCysProProHisSerGlnCysTrpLeuLeuPheArgAsp 1222 | 424 GGGCCAGAGAACCCT410 | 1223 GlyArgCysHisProGlnCysAspSerGluGluCysLeuPheAspGlyTyrAspCysGlu 1242 | 409 CTCGGCTTACAAGCAGGTCCTGAAGAGGATGCAACCTTGACCACTTGTAATTTAT 350 | | 349 TCCTCTTCCAGCTTTGGGCTTGGCCACCCACT | 1255 CysArgAspHisPheHisAsnGlyHisCysGluLysGlyCysAsnAsnAlaGluCysGly 1274 | 316GACAGCACCTCCACACAGCAGCAAAATGGCCAGCTTGGGGAGGCTCCTTCC 260 | | 259 ACGITACTICITGCTITGCGIIGICAGGGGAICTCCGGCCAGAACTGCI 212 | | 211 TTCCTGGAGGTCACGTTCAACGTAAAACAATCGCTGAACACCCGCCCTGTGCATTCAG 152 | :::::: 1314 | 151 ATCCTGATCACCGCCCAGTTCAGTGTGTGTCTTTGGGAAGGTCACTCAGCTGCTTTGAGT 92 | | 91 CTCAGT 86 | 1347 LeuSerGlyAlaArgAspSerSerTrpGluArgGlnAlaProProThrGlnProLeu 1366 | 8585 | ::: 1367 GlyLymGluThrGluSerLeuGlyAlaGlyPheValValMetGlyValAspLeuSer 1386 | 52 GTCCGCGGAAGGGCTTCCTGCAGGCCCAAGGAATCTCCTGGTTGCTGCCCC 2 | |
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    Sequence 565, App
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Sequence 951, App
Sequence 103, App
Sequence 192, App
                                                                                                                                                                                         Sequence 13,
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Shiwei
APPLICANT: Weng, Geath
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TITLE OF INVENTION: Novel Nucleic Acids and
FITLE OF INVENTION: Polypeptides
FILE REFERENCE: 807A
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CURRENT APPLICATION NUMBER: US/10/243,552

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/322,511

PRIOR FILING DATE: 2001-09-13

PRIOR FILING DATE: 2000-12-22

PRIOR PELICATION NUMBER: PCT/US00/35017

PRIOR PLICATION NUMBER: US 09/488,725

PRIOR PPLICATION NUMBER: US 09/552,317

PRIOR PELICATION NUMBER: US 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR PELING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/552,317

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Publication No. US20030224379A1
GENERAL INFORMATION:
      RESULT 1
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

    protein search, using frame_plus_n2p model

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i Sequence 6499, Application US/10106698

j Sequence 6499, Application US/10106698

j Publication No. US2030103690A1

general information

j Publication No. US2030103690A1

general information

j TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

j TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

j CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: US 60/157,137

j PRIOR FILING DATE: 1999-01-03

j PRIOR APPLICATION NUMBER: US 60/157,137

j PRIOR FILING DATE: 1999-11-03

j NUMBER OF SEQ ID NOS: 8564

s SOFTHARE: PatentIn Ver. 3.0

j ERNOTH: 88

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PRIOR PELING DATE: 2000-01-25
PRIOR PRIOR PELING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2000-02-03
PRIOR PELING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR APPLICATION NUMBER: PCT/USO1/04927
PRIOR APPLICATION NUMBER: PCT/USO1/04927
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-02-03
PRIOR FILING DATE: 2001-02-66
PRIOR PILING DATE: 2001-02-66
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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--CysAspThrLeuSer-LysArgSerSerThrSerSerAspHi 990
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CANT: Gerlach, Valerie
CANT: Spaderna, Steven K
CANT: Zerhusen, Bryan
OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
                                                                                                                                     ----GlySerGlnGluSerCysSerAspSerGlyLeuGlyAspHi
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CURRENT APPLICATION NUMBER: US/10/080,334
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/322,712
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/311,980
PRIOR FILING DATE: 2001-09-17
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Padigaru, Muralidhara
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Gusev, Vladimir Y
Casman, Stacie J
Boldog, Ferenc L
Furtak, Katarzyna
Tchernev, Velizar T
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Kekuda, Ramesh
Spytek, Kimberly A
Vernet, Cottine A. M.
Malyankar, Uriel M
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENVIR
FILE REPERCE: 40716 (IP-012)
CURRENT APPLICATION NUMBER: US/10/174,677
CURRENT FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.1
CCACACACACATTTCAGGAACCCCTGAAATAATGCACTATGTCCATGTCCACAGAGTA 842
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827 IleValValIlePheValThrValLeuValArgCysArgHisAlaSerArgPheLysAla
                       1 ProHisThrAspIleSerGlyThrProGluIleMetHisTyrValHisValHisArqVal
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                                                                     Sequence 103, Application US/10174677 Publication No. US20030190704A1 GENERAL INFORMATION:
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1105 erAspAsn-CysTrpMetPro---ProGlyLeuGlyProTyrGlnHisProLys 1121
1077 roasnSeraspGlyProLeuGlyProArg--------
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Shimkers, Richard A.
Gangolli, Esha A.d.
Taupier Jr., Raymond J.
Casman, Stacie J.
Ji, Weizhen
Anderson, David W.
Liete, Mario W.
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Smithson, Glennda
Burgess, Catherine E.
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APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Patturajan, Meera
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Gusev, Vladimir Y.
Li, Li
Vernet, Corine
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Gorman, Linda
Shenoy, Suresh G.
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           PRIOR APPLICATION NUMBER: 60/330,307
PRIOR FILING DATE: 2001-10-18
PRIOR PLILING DATE: 2001-10-38
PRIOR PLILING DATE: 2001-0-3-6
PRIOR PLILING DATE: 2001-0-3-6
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NUMBER OF SEQ ID NOS: 388
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      tThrValAlaGlnSerLeuLeuAlaPheSerThrSerSerSerSerProGlyThrProLe
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                                          APPLICANT: Scrone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: Racbenberg, Mark E.
ITILE OF INVENTION: No. US20040030110Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT APPLICATION NUMBER: 60/281,136
FRIOR APPLICATION NUMBER: 60/281,136
FRIOR PELICATION NUMBER: 60/281,136
FRIOR PELICATION NUMBER: 60/281,906
FRIOR PELICATION NUMBER: 60/281,906
FRIOR PELICATION NUMBER: 60/282,020
FRIOR PELICATION NUMBER: 60/282,930
FRIOR PELICATION NUMBER: 60/282,930
FRIOR FILING DATE: 2001-04-10
FRIOR PELICATION NUMBER: 60/282,930
FRIOR FILING DATE: 2001-04-10
FRIOR APPLICATION NUMBER: 60/283,710
FRIOR FILING DATE: 2001-04-10
FRIOR PELICATION NUMBER: 60/283,710
FRIOR PELICATION NUMBER: 60/283,710
FRIOR FILING DATE: 2001-04-13
FRIOR FILING DATE: 2001-04-13
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Matches:
Conservative:
Mismatches:
Indels:
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Rastelli, Luca
Edinger, Shlomit R.
Stone, David J.
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32.39%
22.48%
1.51%
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Best Local Similarity:
Query Match:
DB:
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| Qy 445GAGAGAATCAGTGCCTTCTTCAGCTCTAIC 474 ::: ::: ::: | QY 475 TGGGACACCATCTTGACCAAGAAGGCATCTACAACACCATCTGCCTGGGAGTC 534 | OY 535 CTCCTGGGCCTGCCACTCTTGGTGATCATCACTCCTCTTCATCTGT 582 :::::: Db talvalphephevalLeuLeuGlyphepheGlyLeuIleLeuHisCysSerSerPheAsn 209 | Qy 583 | RESULT. RES | |
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| | 3989 TGCAGGACTCTTTCTGTGACACAAATGTCCC | 4031 | } | SGULT 7 -10-437-963- Sequence 136 Publication Publication APPLICANT: APPLICAN | • |

us-10-776-827-10.n2p.rapb

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             ---CAACACCATCTGC
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; OTHER INFORMATION: Incyte ID No. US20020187523A1 2267403CD1
US-09-965-528-13
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GENERAL INNORMATION:

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: YUE, Henry

APPLICANT: BURFORD, Neil

APPLICANT: BANDRAN, Oiga

APPLICANT: BANDRAN, Oiga

APPLICANT: BANDRAN, Mariah R.

APPLICANT: BANDRAN, Mariah R.

APPLICANT: BANDRAN, Mariah R.

APPLICANT: BANDRAN, Mariah R.

APPLICANT: BANDRAN, Mariah R.

APPLICANT: BANDRAN, Oiga

APPLICANT: BANDRAN, Oiga

APPLICANT: UJ, DYUNG Aina M.

APPLICANT: UJ, DYUNG Aina M.

APPLICANT: UJ, DYUNG Aina M.

APPLICANT: UJ, DYUNG AINA

FILE REFERENCE: PF-0701 USA

CURRENT APPLICATION NUMBER: 60/134,949

PRIOR APPLICATION NUMBER: 60/134,949

PRIOR APPLICATION NUMBER: 60/144,270

PRIOR PELING DATE: 1999-07-15

PRIOR PELING DATE: 1999-07-15

PRIOR FILING DATE: 1999-07-15

PRIOR PELING DATE: 1999-07-15

SOFTWARE: PER PROGRAM

SEQ ID NOS: 55

SOFTWARE: PER PROGRAM

FERNING DATE: 1999-07-15
        472 ATCTGGGACACCATCTTGACCAAAACACCAAGAAGGCATCTA---
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Publication No. US20020187523A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168997
LENGTH: 1747
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| 171 GlyTrpAspArgPheLeuSerLysHisProlleProPheTyr-----TyrCyslleGly 188
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US-10-437-963-168997
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Indels:
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Matches:
                                                                                                                                                                                                                                                                     Sequence 168997, Application US/10437963; Sequence 168997, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION: APPLICANT: LA ROSA, Thomas J. APPLICANT: Cao, Yongwei; APPLICANT: Cao, Yongwei; APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: BATDAZUK, Brad
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| Db 324 SerGluIleSerSerThrArgCysProLysAlaProGlyArgValLeuValHisThrSer 343 Qy 1089 ACAAATTCAGGTAGCAGGTAGGGGAAGTATATTCTGCTCATCAATGGTCATTGGCT 1148 :: :: ::: Db 344 ValSerProSerProAspAsnLeuArgArgPheAlaLeu | OY 1209 TTGCCAGATTCAGACACATATATACAATTTCCTAACCAGCAGGCCCCCCATACA 1262 :: ::: Db 372 ValLysAspGluGluThrGluAlaGlnArgGlyGluValProGlyProArgProHisSer 391 ON 1263 CCATCTATTCCA 1274 | 392 GlnAsnLeuPro | US-09-946-374-142; Application US/09946374; Sequence 142; Application US/09946374; Publication No. US20030073129A1; GENERAL INFORMATION: | APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L. | | | APPLICANT: ILLIAM, JE APPLICANT: Paoni, JE APPLICANT: Roy, ME APPLICANT: Roy, ME | | APPLICANT: TITLE OF INV | CURREN CURREN CURREN | | FRIOR APPLICATION NUMBER: 60/098750 PRIOR PILING DATE: 1998-09-01 PRIOR PILING DATE: 1998-09-01 PRIOR APPLICATION NUMBER: 60/098803 | ; PRIOR APPLICATION NUMBER: 60/09821 ; PRIOR FILING DATE: 1998-09-02 ; PRIOR FILING DATE: 1998-09-02 ; PRIOR APPLICATION NUMBER: 60/098843 | FRIOR APPLICATION NUMBER: 60/099536 ; PRIOR FILING DATE: 1998-09-09 ; PRIOR FILING DATE: 1998-09-09 ; PRIOR APPLICATION NUMBER: 60/099596 | APPLICATION N FILING DATE: APPLICATION N | ; PRIOR FILING DATE: 1998-09-09; PRIOR APPLICATION NUMBER: 60/099642; PRIOR FILING DATE: 1998-09-09 |
|---|---|---|--|--|--|-----|--|---|---|----------------------------|-----|---|--|---|--|---|
| Alignment Scores: 0.447 Length: 451 Pred. No.: 113.50 Matches: 90 Score: 33.16\$ Conservative: 38 Best Local Similarity: 23.32\$ Mismatches: 124 Query Match: 9.41\$ Indels: 23 Bright Scores: 124 Query Match: 9.41\$ Gaps: 23 | US-10-776-827-10 (1-4460) x US-09-965-528-13 (1-451) QY 318 GTGGCATGCCCAAACCCAAAGGTGGAATAAATTACAAGTGGTCAAGGTTGCATC 377 DD 79 ValHisCysProGlnProValThrGluProGlnGlnCysCys 92 | Qy 378 CTTTTGAGCTCAGGACCTGCTTGTAAGCCGAGAGGGTTCTCTGGC422 Db 93ProLysCysValGluProHisThrProSerGlyLeuArgAlaPro 107 | Qy 423 CCTAATCTAGCCAAGCACCATGGAGAG | Oy 450CAG 467 | Qy 468 CTCTATCTGGGACACCATCTTGACCAAACACCAAGAGGCATCTACAACACCATCTGCCT 527 | 528 | 588 | OY 648 GAAGAAGAAGGATGAAGAAGCCTCTGGATCTCTGCTCAACCAAGCT 695 1:: | Qy 696 TCTCCAGAFGGAGAAGACCATCACTGCCTGTTTAGTTAGGCAGGAAGCAGGTGTTT 755 | 756 CCTTTCT :: | 816 | 858 AACAAACCTCAGACTAAGTGTCCCAGTGGAGGGAGTCCCAGGGACCACGGTGGA | 918 TIGGATACTIGGCAGIATGIGTCCAAIAGCAATGCTCCTTACTGCA | 975 | 1023 | 1029 |

| NUMBER: 60/099741 1. 1998-09-10 NUMBER: 60/099754 1. 1998-09-10 NUMBER: 60/099763 1. 1998-09-10 NUMBER: 60/099792 1. 1998-09-10 NUMBER: 60/099808 1. 1998-09-10 NUMBER: 60/099812 1. 1998-09-10 NUMBER: 60/099812 1. 1998-09-10 NUMBER: 60/099812 1. 1998-09-10 | NUMBER: 60/100388 1998-09-15 NUMBER: 60/100390 1998-09-15 1998-09-15 1998-09-16 1998-09-16 NUMBER: 60/100627 1998-09-16 NUMBER: 60/100664 1998-09-16 NUMBER: 60/100664 1998-09-16 NUMBER: 60/100664 1998-09-16 NUMBER: 60/100648 1998-09-17 NUMBER: 60/100644 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/10084 1998-09-17 NUMBER: 60/100848 1998-09-17 NUMBER: 60/100848 1998-09-17 NUMBER: 60/100849 1998-09-18 NUMBER: 60/100849 1998-09-18 NUMBER: 60/100849 1998-09-18 NUMBER: 60/100849 1998-09-18 | 9-17 60/10101- 60/10106- 9-18 60/10106- 60/10107- 9-22 60/10147- 9-23 9-23 9-23 60/10147- 9-23 60/10147- 9-23 60/10147- 9-23 60/10147- 9-23 60/10147- 9-23 |
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| | QY 1089 ACAAATTCAGGTAGGTACGTGGGCAAGTATATTCTGGTCATCAAATGGTCATTGGCT 1148 :: :: Db 344 ValSerProSerProAspAsnLeuArgPheAlaLeu | 1209 TTGCCAGATTCAC ::: 372 ValLysAepGluC | OY 1263 CCATCTATTCCA 12/4 Db . 392 GlnAsnLeuPro 395 | 12 206-915- ence 282 Ication RAL INFO | ; APPLICANT: Baker, Kevin P. ; APPLICANT: Chen, Jian ; APPLICANT: Desnoyers, Luc ; APPLICANT: Goddard, Audrey | | ; APPLICANT: Watanabe, Colin K. ; APPLICANT: Wood, William I. ; APPLICANT: Annay Zemin ; APPLICANT: Annay Zemin ; TITLE OF TRUNDANTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC | ; TITLE OF INVENTION: ACIDS ENCODING THE SAME ; FILE REFERENCE: P3430R.C513 ; CURRENT APPLICATION UNDER: US/10/206,915 ; CURRENT FILING DATE: 2002-07-26 | ; PRIOR APPLICATION NUMBER: 10/052586 ; PRIOR FILING DATE: 2002-01-15 ; PRIOR APPLICATION NUMBER: 60/059263 ; PRIOR PRIVIC DATE: 1997-09-18 | ; PRIOR APPLICATION NUMBER: 60/059266 ; PRIOR FILING DATE: 1997-09-18 ; PRIOR FILING DATE: 1997-10-17 | ; PRIOR APPLICATION NUMBER: 60/063120 ; PRIOR FILING DATE: 1997-10-24 ; PRIOR APPLICATION NUMBER: 60/063121 ; PRIOR PTI-ING DATE: 1997-10-24 | | | | 15.E. | Alignment Scores: 0.447 Length: 451 Pred. No.: 113.50 Matches: 90 Score: 33.16% Conservative: 38 Best Local Similarity: 23.32% Mismatches: 124 |
|---------------------------------------|--|---|--|---|--|--|---|--|--|---|---|---|---|--|-------|--|
| ; PRIOR APPLICATION NUMBER: 60/105807 | Alignment Scores: Pred. No.: Score: Score: Pred. No.: 113.50 Matches: Percent Similarity: Best Local Similarity: 23.32\$ Mismatches: 134 Query Match: 1018 Gaps: 23 | US-10-776-827-10 (1-4460) x US-09-946-374-142 (1-451) QY 318 GTGGCATGCCCAAACCCAAAGCTGGAATAATTACAAGTGGTCAAGGTTGCATC 377 Qy | 378 CTTTTGAGCTCAGGCTGCTTGTAAGCCGAGAGGCTTCTCTGGC 93ProLyscysValGlubroHisThrProSerGlyLeuArgA | Qy 423 CCTAATCTAGCCAAGCAC | Qy 450CAG 467 | Qy 468 CTCTATCTGGGACACCATCTTGACCAAACACCAAGAAGCATCTACAACACCATCTGCCT 527 | Qy 528 GGGAGTCCTCCTGGGCCTGCCACTCTTGGTGATCATCACACTCCTCTTCATCTTTGCA 587 | OY 588 TTGCTGCTGCACCACCAGGAAGAGGGGCCAGCAGCAGAGAAAAAAAA | Qy 648 GAAGAAGAAGGATGAAGAAGACTCTGGATCTCTGCTCAACCCAAGCT 695 ::: | Qy 696 TCTCCAGATGGAGAACCATCACTGCCTGTTTAGTTAGGCAGGAAGCAGAGGTGTTT 755 ::: :::: | Oy 756 CCTTTCTGGGGCTAAGCCTCCTTCTGACCACACAGACATTTCAGGAACCCCTGAAATA 815 | Qy 816 ATGCACTATGTCCACAGAGTAACTACTCAACCAAGG 857 | QY 858 AACAAACCTCAGACTAAAGTGTCCCAGTGGAGGGAGTCCCAGGGACCACGTGGAATTC 917 | Qy 918 TTGGATACTGTCTTGGCAGCTATGTGTCCAATAGCAATGCTCCTTACTGCAGACCCA 974 | 975 | Qy 1023 GAACAT 1028 |

| Qy 1149 ATGTACTTTGTGCAGGAAGTACATTATCTACAGTCACAAAAATGTCTCATGGGAAAGCC 1208 Db 357GluHisGluAlaSerAspLeuValGluIleTyrLeuTrpLysLeu 371 Qy 1209 TTGCCAGATTCAGACACATATAGAATTTCCTAACCAGCAAGGCCCCCATACA 1262 Db 372 VallysAspGluGluThxGluAlaGlnArgGlyGluValProGlyProArgProHisSer 391 Qy 1263 CCATCTATTCA 1274 Bb 392 GlnAsnLeuPro 395 | RESULT 13 US-10-199-670-282 // Sequence 282, Application US/10199670 // Publication No. US20040033560Al // GENERAL IMPORMATION: // APPLICANT: Baker, Kevin P. // APPLICANT: Desnoyers, Luc // APPLICANT: Goddard, Audrey // APPLICANT: Gordowski, Paul J. // APPLICANT: Gurney, Austin L. // APPLICANT: Gurney, Austin L. // APPLICANT: Pan, James // APPLICANT: Pan, James // APPLICANT: Pan, James // APPLICANT: Pan, James // APPLICANT: Pan, James // APPLICANT: Pan, James | APPLICANT: Wood, William I. APPLICANT: Wood, William I. APPLICANT: AND ZEMENT APPLICANT: APPLICANT: ACADS ZEMENT ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITILE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P34.30RL401 CURRENT APPLICATION NUMBER: US/10/199,670 CURRENT FILING DATE: 2002-07-19 PRIOR FILING DATE: 1997-09-18 PRIOR FILING DATE: 1997-09-18 PRIOR PELICATION NUMBER: 60/069266 PRIOR FILING DATE: 1997-09-18 PRIOR APPLICATION NUMBER: 60/062260 PRIOR APPLICATION NUMBER: 60/062260 PRIOR APPLICATION NUMBER: 60/062260 PRIOR APPLICATION NUMBER: 60/062260 PRIOR APPLICATION NUMBER: 60/062260 | PRIOR FILING DATE: 1997-10-24 PRIOR PEDLICATION NUMBER: 60/063121 PRIOR PEDLICATION NUMBER: 60/063486 PRIOR PELING DATE: 1997-10-24 PRIOR APPLICATION NUMBER: 60/063540 PRIOR PELING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR APPLICATION NUMBER: 60/063541 PRIOR APPLICATION NUMBER: 60/063541 PRIOR APPLICATION NUMBER: 60/063541 PRIOR APPLICATION NUMBER: 60/063544 PRIOR APPLICATION NUMBER: 60/063544 PRIOR PLING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-28 | Alignment Scores: |
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| | CCTAATCTAG | | AAGG L LysG ATTC UVal CCCA CCCA CCAAA | 1023 GAACAT 1028 |

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| 19 ValHisCysProGlnPro | 1023 GAACAT 1028 1029 TATCATACATACATCCCAAGTGTGTGCACATGCACACACA |

| ProLysSerCysGlnHi | ProLysSerCysGlnHisAsnGlyThrMetTyrGlnHisGlyGluIlePheSerAlaHis 127 | ; Sequence 13, Appl ; Publication No. U ; GENERAL INFORMATI ; APPLICANT: INCYT ; APPLICANT: TANC |
|--|--|--|
| CTCTATCTGGGACACCA::: :: IleTyrCysGly | CTCTATTGGGACACCATCTTGACCAAACACGAAGAAGCATCTACAACACCATCTGCCT 527 | ; APPLICANT: YOE, ; APPLICANT: LAL, ; APPLICANT: BURE; ; APPLICANT: BANG |
| GGGAGTCCTCCTGGGCC7 | GGGAGTCCTCCTGGGCCTGCCACTCTTGGTGATCATCACACTCCTCTTCATCTGTTGCCA 587 | ; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF INV |
| TTGCTGCTGCACCACCAGGCAAGAGG ::: SerCysCysGlnAlaCysLysAspGlu- | TTGCTGCTGGAGCCCACGAGAAGAGGGCCAGCCAGGCAGAGAAAAAAA | ; FILE REFERE ; CURRENT APP ; CURRENT FIL: ; PRIOR APPLI |
| GAAGAA | 648 GAAGAAGAAGGATGAAGAAGACCTCTGGATCTCTGCTCAACCCAAGCT 695 | ; PRIOR FILING DAT ; NUMBER OF SEQ II ; SOFTWARE: PERL F ; SEQ ID NO 13 |
| TCTCCAGATGGAGAAGAG; ::: :::: 31y-ArgLysArgGl; | TCTCCAGATGGAGAAGAGCCATCACTGCCTGTTTAGTTAG | ; TYPE: PRT ; TYPE: PRT ; ORGANISM: HOMO ; FEATURE: |
| CCTTTCTGGGGCTAAGCC ::: erPheIle | CCTTTCTGGGGCTAAGCCTCCTTCTGACCACACAGACATTTCAGGAACCCCTGAAATA 815 :: erPhelle231 | ; NAME/KEY: misc ; OTHER INFORMATI US-09-969-984-13 |
| ATGCACTATGTCCATGTC | ATGCACTATGTCCACAGAGTAACTACTCAACCAAGG 857 | Alignment Scores Pred. No.: Score: Percent Similarit |
| AACAAACCTCAGACTAAG7 u-LysHisLysLysAlaC | AACAAACCTCAGACTAAGTGTCCCAGTGGAGGGGAGTCCCAGGGACCACGTGGACAATTC 917 ::: | Best Local Similari Query Match: DB: |
| TTGGATACTGTCTTGGCAG | | US-10-776-827-10 (1 Qy 318 GTGGC |
| GGCATGCCTCCCGLVArgGlnAspCvsGlnA | | Db 79 |
| GAA | | |
| 3 uLysValAlaG yLysC TATCCATACATCTCAATA | GlubysValalaGlyLysCysCysLysIleCysProGluAspLysAlaAspProGlyHis 323 TTATCCATACATCTCAATATGGTTCCCAAGTGTGTGTAGTAGTGTGTAGTAGTAGAGTAAAAAAAA | Oy 423 Db 108 |
| | | Qy 450 |
| ACAAATTCAGGTAGCAGGT/ ::: /alSerProSerProAspa | ACAAATTCAGGTAGCAGGTACGTGGGGAAGTATATTCTGCTCATCAAATGGTCATTGGCT 1148 ::: ::: ::: ValSetProAenAenLenaratophealalan. | a ko |
| ATGTACTTTGTGCAGGGAA(| AIGTACTTTGIGCAGGGAAGTACATTATCTACAGTCACAAAATGTCTCATGGGAAAGCC 1208 | Db 148 |
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| GlnAsnLeuPro 395 | | Oy 648 |
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spSerValGlnSerLeuHisGlyValArgHisProGlnAspProCysSerSerAspAla 205
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ATTERSON, Chandra
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S: PF-0701-1 USA
DATE: 2001-10-02
TATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
TATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
PROGRAM
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PURPLE: 1999-10-10-04
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UE, Henry
AL, Preeti
URFORD, Neil
ANDMAN, Olga
AUGHN, Mariah R.
ZIMZAI, Yalda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 CCTTTCTGGGGGCTAAGCCTCCTTCTGACCACACACACTTTCAGGAACCCCTGAAATA 815
                                                                                                                                             858 AACAAACCICAGACTAAGIGICCCAGIGGAGGGCAGICCCAGGGACCACGIGGACAAIIC 917
                                                                                                                                                               918 ITGGATACTGTCTTGGCAGCTATGTGTCCAATA---GCAATGCTCCTTACTGCAGACCCA 974
                                                                                                                                                                                                                   265 TrpHisProAlaPheArgAlaPheGlybroLeuProCysIleLeuCysThrCysGluAsp 284
                                                                                         816 ATGCACTATGTCCATGTCCACAGAGTAACTACTCAACC-------AAGG 857
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232 -------ProlysGlyAlaGlySerThrThrValLysIleValLeuLysG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                     206 Gly-Arg---LysArgGlyProGlyThrProAlaProThrGlyLeu-SerAlaProLeuS
                                                              -----ProArgHisPheArg-
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392 GlnAsnLeuPro 395
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Search completed: September 21, 2004, 16:53:47 Job time : 498 secs

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30, Appl 34, Appl 28, Appl 28, Appl 26, Appl 26, Appl 26, Appl 26, Appl 26, Appl 28, Appl 28, Appl

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NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCURTENTLY HERWITH
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
                               US-08-452-654-2

US-08-452-658-2

US-08-452-655B-7

US-08-450-658-7

US-08-450-582-7

US-08-450-582-7

US-08-450-582-7

US-08-450-582-7

US-08-450-582-7

US-09-136-605-7

US-09-136-605-7

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US-09-252-991A-25051

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US-09-26-2550-91A-25051

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US-09-252-991A-24513

US-08-326-592-8

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US-08-326-592-991A-20267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Yamagata, Kazuya
APPLICANT: Adisaki, Pamela
APPLICANT: Furuta, Pamela
APPLICANT: Furuta, Hiroto
APPLICANT: Horikawa, Yukio
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIJ
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 127, Application US/08927219
; Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.O. Box 4433
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
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Houston
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Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgnZ_1/USFPTO_spool_p/USI0776827/runat_21092004_133241_20811/app_query.fasta_1.4615
-DB=IS8used_Patenrs_AA - QFWT=fastan -SUFFIX=n2p.rai - mINMATCH=0.1 L-COPCL=0
-LOOPEXN=0 -UNITS-EDIts -START=1 -RND=-1 - MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-USER=USI076827_@CGN_1 _1 119 @-unat_21092004_133241_20811 -NCUP=6 -ICFU=3
-NO_MMAP -LAKCEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO_MMAP -LAKCEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2, Appli
Sequence 31030, A
Sequence 6, Appli
Sequence 5, Appli
Sequence 23962, A
Sequence 7, Appli
Sequence 7, Appli
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Sequence 7, Appli
                                                                                                                   September 21, 2004, 15:10:50 ; Search time 72.5 Seconds (without alignments) 6351.775 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                  - protein search, using frame_plus_n2p model
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US-08-927-219-127
US-08-927-219-4
US-09-252-91A-31030
US-09-798-051-5
US-09-798-051-5
US-09-252-991A-33046
US-09-252-991A-33046
US-09-252-991A-33046
US-09-252-991A-33047
US-08-49-731-7
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Jatabase :

Result

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APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisha
APPLICANT: Masisaki, Pamela J.
APPLICANT: Horikawa, Yukio
APPLICANT: Horikawa, Yukio
APPLICANT: Horikawa, Yukio
APPLICANT: Morzel, Stephen
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1134 AAATGGTCATTGGCTATGTACTTTGTGCAGGAAGTACATTATCTACAGTCACAAAAATG 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGAACATTTATCC-----ATACATCTCAATATGGTTCCCAAGTGTGTGCACATGCAC 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1074 GTAACACACACACACACAAATTCAGGTAGCAGGTACGTGGGCAAGTATATTCTGCTCATC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485
                                                     387 HisserLeuGluGlnThrSerProGlyLeuAsnGlnGlnProGlnAsnLeuIleMetAla 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1194 TCTCATGGGAAAGCCTTGCCAGATTCAGACACATATATACAATTTCCTAACCAGCAAGGC
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     GTAACTACTCAACCAAGGAACAAACCTCAGACT
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08927219
Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1362 AGCAACCIGCTACAGICC 1379
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228 GluArg---GluThrLeuValGluGluCys-----
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APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: 37,259
TELECHONIUNICATION INFORMATION:
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                                                               --CAAGCTICTCCAGATGGAGAAGAGACC 716
                                                                                     338 GlyProLeuValThrValSerThrProLeuHisGlnValSerProThrGlyLeuGluPro 357
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387 SerLeuGluGlnThrSerProGlyLeuAsnGlnGlnProGlnAsnLeuIleMetAlaSer 406
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       320 ValArgGlyGlnProAlaThrSerGluThrAlaGluValProSerSerSerGly-----
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407 Leubro---GlyValMetThrIleGlyProGlyGluProAlaSerLeuGlyProThrPhe
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Patent No. 6187533
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                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                       ARCD: 272
                                                                                                                                                                                                                                                                                         NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        630 amino acids
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113.00
31.61%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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1023 GAACATTTATCC-----ATACATCTCCAATATGGTTCCCAAGTGTGTGCACATGCACGTA 1076
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537 ProThrlysGlnValPheThrSerAspThr-----GluAlaSerSerGluSerGlyLeu 554
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105 CCGAGAGGTTTCTCTGGCCCTAATCTAGCCAAGCACCATGGAGAGAATCAGTGCCTTCTT 464
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387 SerLeuGluGlnThrSerProGlyLeuAsnGlnGlnProGlnAsnLeuIleMetAlaSer
                    CAGCTCTATCTGGGACACCCATCTTGACCAAACACCAAGAAGGCATCTACAACACCATCTG
                                                                                                                                                                                      558 GATCATCACACTCCTCTTCATCTGTTGCCATTGCTGGAGCCCACCAGGCGAAGAGGG
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APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBLLITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGAATAAATTACAAGTGGTCAAGGTTGCATCCTTTTGAGCTCAGGACCTGCTTGTAAG 404
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Vourrent Application Data:
APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith CLASSIFICATION: 435
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APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
                                                                                                                                                                                                         Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  Kaisaki, Pamela J.
Furuta, Hiroto
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                    Bell, Graeme I.
Yamagata, Kazuya
Oda, Naohisha
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
        GENERAL INFORMATION:
                                                                                                                                                                                                                                        CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                        Houston
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STREET: P.
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| | Alignment Scores: Pred. No.: Cores: Cores: Best Local Similarity: Cuery Match: 1.36* US-10-776-827-10 (1-4460) x US-09-798-051-6 (1-408) | Qy 318 GTGGCATGCCCAAACCCAAAGCTGGAAGTAAATTACAAGTGGTCAAGGTTGCATC 377 Db 58 ValHisCysProGlnPro |
|---|---|---|
| OY 1257 CATACACCATCTATTCCATAAACCACTCAGGTTACAGATGCATGC | US-09-252-991A-31030 Alignment Scores: 0.0233 Length: 180 Score: 109.00 Matches: 50 Percent Similarity: 39.46\$ Conservative: 23 Best Local Similarity: 27.03\$ Mismatches: 62 Ouery Match: 1.36\$ Gaps: 9 | MACACGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA |

| Query Match: 1.36% Indels: 135 DB: 4 Gaps: 23 US-10-776-827-10 (1-4460) x US-09-798-051-5 (1-429) (1-420) 318 GTGGCATGCCCAAACCCAAAGCTGGAAGAGAATTACAAGTGGTCAAGGTTGCATC 377 QY 318 GTGGCATGCCCAAACCCAAAGCTGGAAGAGAATTACAAGTGGTCAAGGTTGCATC 377 | | 528 GGGAGTCCTCCTGGGCTGCCACTCTTGGTGATCACTCCTCTTCATCTGTTGCCA 587 | | 232ProlysishladlySerThrThrVallysileValleud 858 AACAAACCTCAGACTAAGTGTCCCAGTGGAGGCACTCCCAGGGACCACGTGGACAA 858 AACAAACCTCAGACTAAGTGTCCCAGTGGAGGGCACTCCCAGGGACCACGTGGACAA 246 lu-LySHisLySalacysValHisGlyGlyLySThrTyrSerHisGlyGli 246 lu-LySHisLySalacysValHisGlyGlyLySThrTyrSerHisGlyGly 918 TTGGATACTGTCTGGCAGCTATGTGCCAATAGCAATGCTCCTTACTGCAGA 918 TTGGATACTGTCTTGGCAGATGTAGCAATGCTCCTTACTGCAGA 919 GGCATGCCTCCCACCTGTCTCTGGCAATGCTCTACTGCAAAGCA 975 GGCATGCCTCCCACCTGTCTCTGGCAAAGCA 975 GGCATGCCTCCCACCTGTCTCTGGCAAAGCA 976 GGAATGCCTCCCACCTGTCTCTGGCAAAGCA 977 GGCATGCTCCC | 1023 GAA |
|--|-----------|--|---|---|---------------------------|
| Query P DB: US-10-' Qy | 8 8 8 8 8 | 8 8 8 8 | 96 & 96 & 96 & 96 & 96 & 96 & 96 & 96 & | 8 28 28 28 28 | 3 4 5 6 6 |
| 696 TCTCCAGATGGAGAGACCATCACTGCCTGTTTAGTTAGGCAGGAAGCAGAGGTGTTT 755 185 Gly-ArgLysArgGlyProGlyThrProAlaProThrGlyLeu-SerAlaProLeuS 203 756 CCTTCTGGGGCTAAGCCTCTTCTGACCACACACATTCAGGAACCCTGAAATA 815 [| | 1023 GAA | | Db 377 LeuLeuAlaGlyPrOHis 382 KESULT 6 VS-09-798-051-5 Sequence 5, Application US/09798051 Sequence 5, Application US/09798051 Sequence 5, Application US/09798051 Sequence 5, Application US/09798051 Septent No. 6622780 APPLICANT: Cam, Linh APPLICANT: Cam, Linh APPLICANT: Cam, Linh APPLICANT: Cam, Chordin-Like-2 Molecules and Uses Thereof TITLE REFERENCE: 01-005 CURRENT APPLICATION NUMBER: US/09/798,051 CURRENT APPLICATION DATE: 2001-03-05 | WOMBER OF SEQ ID NOS: 21 |

| | Db 564 nbrohlangGinbroGin |
|--|---------------------------|
| Oy 1128CTCATCAAATGGCCATTGGCTATGTACTTGTGCAGGAAGTACTTATCTACA 1181 Db 364 ValGluileTyrLeuTrpLysLeuValLysGly1lePheHisLeuThrdInileLysLys 383 Oy 1182 GTCACAAAATGTCTCATGGGAAAGCCTTGCCAGATTCAGACATATATCTT 1241 Db 384 ValArglysGlAapPheGlirysGlAalaGln | Alignment Scores: |

| TGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | ORIGINAL SOURCE: ORGANISM: Homo IMMEDIATE SOURCE: CLONE: APC US-07-741-940-7 Alignment Scores: Pered. No.: Score: Percent Similarity: Percent Similarity: Best Local Similarity: Dest Local Similarity: Cuery Match: DB: US-10-776-827-10 (1-44 QY 2797 TCACATAA | MOLECULE TYPE: prot ORIGINAL SOURCE: ORGANISM: Homo sc IMMEDIATE SOURCE: CLONE: APC -741-940-7 No.: No.: Int Similarity: Local Similarity: Match: Match: Apt TCACATAACA 2797 TCACATAACA |
|---|--|---|
| | Oy 2857 Db 2244 Qy 2917 Db 2280 Qy 2995 Db 2300 Qy 3052 Db 2313 Qy 3100 Qy 3130 Db 2313 Db 23330 | CCCCACAACT ::: ProvalSerL CCCTAGAATG |
| NUMBER OF SEQUENCES: 94 CORRESPONDENCES: 94 CORRESPONDENCES: 94 STREET: 1001 G Street, NW CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20001-4598 COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: BAFENIA RElease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATE: 19920109 CLASSIFICATION NUMBER: US/07/741,940 FILING DATE: 19920109 CLASSIFICATION NUMBER: US/07/741,940 FILING DATE: 19920109 CLASSIFICATION NUMBER: 105.07/741,940 FILING DATE: 19920109 TELESPROKENCE CASO STATE REGISTRATION NUMBER: 1107.035574 TELECOMMUNICATION INFORMATION: TELEPRAX: 202-508-9299 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: | | |

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...-GAAAGGAGCCTAAGGCCATTGTTG 3360
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rSerThrLysSerSerGlySerGluSerAspArgSerGluArgProValLeu 2436
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yLeuAsnGlnMetAsnAsnGlyAsnGlyAlaAsnLysLysValGluLeuSer 2416
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rAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly 2369
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-GlnGlnProLeuSerArgProlleGlnSerProGlyArgAsnSerlleSer 2329
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uGlyGlnThrAlaThrThrSerProArgGlyAlaLysProSerValLysSer 2279
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|2350 ProSerThrAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly 2369
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                        US-10-776-827-10 (1-4460) x US-08-289-548A-7 (1-2842)
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2493 rThrHisSerSer 2497
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                                                                                          2473 OThrArgSerGlnAlaGlnThrProValLeuSerProSerLeuProAspMetSerLeuSe 2493
                                     -----ArgProAlaSerPr 2473
----TCCATGTTTTATGCTTCTCTGATTCCCTCTTCTGCCTGCACCAGACCAGCC---CC 3453
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAMERA, YUSUKE
APPLICANT: THIJVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
HUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
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75
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105
92
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COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,548A
FILLING DATE: 12-AUG-1994
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                        SEE: Banner & Allegretti, LTD : 1001 G Street, NW Washington
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ER: 1107.46943
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APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, WARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, PHILIP J.
APPLICANT: KINZLER, KENNETH
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                  Sequence 7, Application US/08289548A Patent No. 5648212
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NAME: RAGAN, SATAN A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9299
                                                                                                                                         3514 AACCCATGGGACC 3526
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106.50
35.41%
24.59%
1.33%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                         2280 GluleuSerProValAlaArgGlnThrSerGlnIleĠlyĠlySerSerLysAlaProSer 2299
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2417 ArgMetSerSerThrLysSerSerGlySerGluSerAspArgSerGluArgProValLeu
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                                                          3052 GAATTAAGACAGCAGTCAGTTGTCATTGCCATGACAAGGCCT------CTATCT
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CORRESPONDENCE ADDRESS:
ADDRESSEE Banner & Allegretti, LTD
STREET: 1001 G Street, NW
GGAGGGCGGATC-
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NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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ANAND, RAKESH
CARLSON, MARY
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HEDGE, PHILIP J.
JOSLYN, GEOFF
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2493 rThrHisSerSer 2497
   2977 GATCIA
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            APPLICANT: CARLSON, WARY
APPLICANT: CARLSON, WARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HOSLYN, GEOFF
APPLICANT: ANINLER, KENNETH
APPLICANT: MAKAMURA, YUSUKE
APPLICANT: THILIVERIAM, ALEXANDER F.
APPLICANT: THILIVERIAM, ALEXANDER F.
APPLICANT: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2842
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33
105
92
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION: 536
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Conservative:
Mismatches:
Indels:
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1001 G Street, NW
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2842 amino acids
TYPE: amino acid
STRANDEDNESS: single
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106.50
35.41%
24.59%
1.33%
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               ADDRESSEE:
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2330 ProGlyArgAsnGlyIleSerProProAsnLysLeuSerGlnLeuProArgThrSerSer 2349
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2350 ProSerThrAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly 2369
                                                                                                                                                                            3181 ---CAGTCACTTCCACAGCCGATGACTCAGAAGAGCCAAAACCCAGAATGGGGCCTCTT 3237
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2437 ValArgGinSerThrPheIleLysGluAlaProSerProThr-LeuArgArgLysLeuGl 2456
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                                                                                                                                                                                                                  3238 TICCCCATCACAGACTCCCCTGACAACCTTTCCTGGCGTAACTAGAGGAGTCCCAGTGCA
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APPLICANT: CARLSON, MARY
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: NINZLER, KENNETH
APPLICANT: NAKAMURA, YUGUKE
APPLICANT: NAKAMURA, YUGUKE
APPLICANT: THILIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3361 ATA-----TCCACTCTTTTTTCCACTTCCTTCTCATCTTTTTC---
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CURRENT APPLICATION DATA:
CHELICATION NUMBER: US/07/741,940
FILING DATE: 19920109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Banner, Birch, McKie & Beckett
!: 1001 G Street, NW
Washington
                                                              3148 CCCCAGGGATGAAACACCCCAGAAACTCACTTC1
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Patent No. 5352775
GENERAL INFORMATION:
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Compatible OPERATING SYSTEM: PC-DOC'S SOFTWARE: Party PDE STORY PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSI
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2493 rThrHisSerSer 2497
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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------GlnGlnProLeuSerArgProlleGlnSerProGlyArgAsnSerlleSer 2329
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/08/449,731
FILING DATE: 25-May-1995
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION TOWNER: 08/289,548
APPLICATION NUMBER: 08/289,548
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 32,141
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-776-827-10 (1-4460) x US-08-449-731-7 (1-2842)
                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
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106.50
35.41%
24.59%
1.33%
               STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
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Best Local Similarity:
Query Match:
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2474
                                                3454 AGCCCTTTATTCCTCTCTCTTTTCACTCCTTCCAGCCTCTGTGTACTGCCACTGGC 3513
::: ||||||| valargGlnSerThrPhelleLysGluAlaProSerProThr-LeuArgArgLysLeuGl 2457
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ALBERTSEN, HANS
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THIVERES, KENNETH
APPLICANT: THIVERES, ANDREW
ITTLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,548A

FILING DATE: 12-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kagan: Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 1107.46943

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAK: 202-508-9100

TELEFAK: 202-508-9109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                              RESULT 14
10S-08-289-548A-2
1 Sequence 2, Application US/08289548A
1 Patent No. 5648212...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEAR: 202-500 INCOMMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTER.STICS: SEQUENCE CHARACTER.STICS: TWOTH: 2843 anino acids
                                                                                                                                                                                                    3514 AACCCATGGGACC 3526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
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2351 ProserThrAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly 2370
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2281 GluLeuSerProValAlaArgGlnThrSerGlnIleGlyGlySerSerLysAlaProSer 2300
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2398 SerLysGlyLeuAsnGlnMetAsnAsnGlyAsnGlyAlaAsnLysLysValGluLeuSer
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|2225 SerargGlyargThrMet11eHis11eProGlyValArgAsnSerSerSerSerThrSer
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                              Indels:
                      NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION:
TELEPHONE: 202-508-9100
TELEPAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                 TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    : 2843 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                         0.228
106.50
35.41%
24.59%
1.33%
                                                                                                                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: protein
US-07-741-940-2
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TCACATAACAGAATAACTTGCCATCTGCCTGCACCAAACCCAGGGATGTGGAAGACATCT
                                                       CCCCACACTGCCACTGCTCACCAGGACAAGCTGCCCTTTCCTGTCTCCACCTCTCAGTCC
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US-08-452-654-2
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Sequence 2, Application US/08452654
Patent No. 5691654
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY

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2797 TCACATAACAGAATAACTTGCCATCTGCCTGCACCAAACCCAGGGATGTGGGAAGACATCT 2856
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2245 ProValSerLysLysGlyProPro-------LeuLysThrProAlaSerLysSer 2260
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| GluLeuSerProValAlaArgGlnThrSerGlnIleGlyGlySerSerLyBAlaProSer
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APPLICANT: HEDGE, PHILIP J.
APPLICANT: MINZLER, KENNETH
APPLICANT: MINZLER, KENNETH
APPLICANT: MAKAMURA, YUSUKE
APPLICANT: MAKAMURA, YUSUKE
APPLICANT: THIIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                              3: Banner, Birch, McKie & Beckett
1001 G Street, NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECHWUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: Rloppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2843 amino acids
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35.41%
24.59%
1.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-452-654-2
                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                COUNTRY: USA
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Pred. No.:
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| QQ | 2351 ProSerThrAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly 2370 |
| ò | 3181CAGTCACTTCCACAGCCGATGACTCAGAAGAGCCAAACCCAGAATGGGGCCTCTCTT 3237 |
| QQ | 2371 ArgGlnMetSerGlnGlnAsnLeuThrLysGlnThrGlyLeuSerLysAsnAlaSerSer 2390 |
| ò | |
| q | 2391 IleProArgserGluserAla 2397 |
| δλ | 3298 GGAIAGGCCCTAAACGTTTTGTTAAATAAACAGGTGCAT 3336 |
| qa | 2398 SerLysGlyLeuAsnGlnMetAsnAsnGlyAsnGlyAlaAsnIysLysValGluLeuSer 2417 |
| ò | |
| q | 2418 ArgMetSerSerThrLysSerSerGlySerGluSerAspArgSerGluArgProValleu 2437 |
| δ | 3361 ATATCGACTCTCTTTCCACTTCCTTCTCATCTTTTC3400 |
| qa | ::: 2438 ValargGlnSerThrPheIleLysGlualaProSerProThr-LeuArgArgLysLeuGl 2457 |
| ò | 3401TCGATGTTTTATGCTTCTGATTCCCTCTTCTGCACCAGCCAG |
| qa | 2457 uGluserPlaserPheGluserLeuserProserSerArgProAlaserPr 2474 |
| δλ | 3454 AGCCCTTTATTCCTCTCCATTTCACTCCAGCCTCTGTCCCTGAACTGCCACTGGC 3513 |
| qq | 2474 oThrArgSerGlnAlaGlnThrProValLeuSerProSerLeuProAspMetSerLeuSe 2494 |
| ò | 3514 AACCCAIGGGACC 3526 |
| QU | 2494 rThrHisSerSer 2498 |
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Search completed: September 21, 2004, 15:48:20 Job time : 196.5 secs

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Q8cgb6 mus musculu Q8xsv8 bos taurus Q8xsv8 bos taurus Q7z5j3 homo sapien Q8vdc2 mus musculu Q8cg65 mus musculu Q8cg1 arabidopsis Q8ct0t drosophila Q9fmj2 arabidopsis Q8llr5 rattus norv Q9wv18 mus musculu Q96kw2 homo sapien Q8ndx5 homo sapien Q8ndx5 homo sapien Q8ndx5 homo sapien Q8ndx5 homo sapien Q8ndx5 homo sapien
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Q8bh09 mus musculu
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"Analysis of the mouse transcriptome based on functional annotation of
60,700 full-length CNNAs.";
Nature 420:563-573 (2002).
EMBL; AK028922; BAC26196.1; -.
SEQUENCE 126 AA; 14102 MW; CEB01EF3E6C50A44 CRC64;
                                                               Q9hc56 homo
     28cbl2 mus
                    Q8ww72 homo
Q9d4t5 mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Q99LH4
Q8CJ95
Q8CGB6
Q9XSV8
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Q7Z5J3
Q8VDC2
Q8IZC6
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Q8CHP6
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Q9WVL8
                                 29D4T5
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Q9HC56
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TRAIN-ESTBL/66; TISSUE-SKin;
MEDLINE-22354683; Pubmed=12466851;
The FANTOM CORBOTLUM:
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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NCBI_TaxID=10090;
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-Q=/CGn2 1/USFTO spool p/US10776827/runat_21092004_133240_20778/app_guery.fasta_1.4615
-Q=/CGn2 1/USFTO spool p/US10776827/runat_2109204_133240_20778-lunaphumaad.cdi
-LOOPEXT=0. -UNITG=bits -START=1 -END=1 - MATRIX=blosum62 - TRANS=humad.0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-1 -MATRIX=blosum62 - TRANS=humad.0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-1 -THR_MAX=100 -THR_MIN=0 -ALIGN=-5
-USFR=-USI0776-FY=-pto -NORM=-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                             September 21, 2004, 15:06:59 ; Search time 410 Seconds (without alignments) 6864.445 Million cell updates/sec
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     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                 - protein search, using frame_plus_n2p model
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1085 ACACACAAATTCAGGTAGCAGGTACGTGGGCAAGTATATTCTGCTCATCAAATGGTCATT 1144
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LysThrSerGlySerLeuLeuSerProSerSerSerArgTrpArgArgAspHisHisCys
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-2002) to the El
EMBL; BC020789; AAH20789.1; -
Hypothetical protein.
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SEQUENCE 62 AA; 6816 MW;
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                                                                                                                                                                                                                                        STRAINS 2235468; PubMed=12466851; MEDLINE=2235468; PubMed=12466851; The FIANTOM Consortium, Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDMAs."; Nature 420:563-573 (2002). BRENE, RAC35614; BAC291961; - SEMBL, RAC35614; BAC291961; - SEQUENCE 160 AA; 18109 MW; 9E43AlAB200AAE9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TOBI TaxID=10090;
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gAspLeuGluGluProLeu 125
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01-MAR-2003 (TrEMBLrel. 23,
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Unclassifiable.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 AGTGGCAGGCCCAGGAGGACTCCCAGGCAGATGGTGTTGTAGATGCCTTCTTGGTGTTTG 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGlyAsnProArgSerThrAlaArgGlnThrValleuLysThrProLeuSerCysLeu 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GICAAGAIGGIGICCCAGAIAGAGCIGAAGAAGGCACTGAIICICCCAIGGIGCII 435
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                 Last sequence update)
Last annotation update)
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01-0CT-2003 (TEMBLrel. 25, Created)
01-0CT-2003 (TEMBLrel. 25, Last sequence update)
01-0CT-2003 (TEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686L0546.
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Conservative:
Mismatches:
                                                            122 AA
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                                                                                                               Created)
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EMBL; AK016191; BAB30142.1; -.
MGD; MGI:1922505; 4930562F07Rik.
                                                                  090475;
01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001)
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4930562F07RIK.
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496 CACCAAGAAGCATCTACAACACCATCTGCCTGGGAGTCCTCCTGGGCCTGCCACTCTTG 555
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                                                                                                                                                   Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BX537422, CAD97664.1; --
Hypothetical protein.

SRQUENCE 1203 AA; 132214 MW; 25B905E7E6203F10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          847 AlaGlnArgSerLysGlnGlyAlaGluTrpMetSerProAsnGlnGluAsnLysGlnAsn
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887 IleGlu--GluSerLysProAspAspAlaValHisGluProIleAsnGlyThrIleSerL
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960 LysHisHisValIleGlnGluLeuProLeuAspAsnThrPheValGlyGly------
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mismatches:
Indels:
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Matches:
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38.23%
22.71%
1.61%
                                                                                                                                FISSUE=Human amygdala;
(Human)
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Best Local Similarity:
                                                                                                        SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=9606;
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1037 sGluProValGlySerGlyThrLeulleSerHis-ProLeuProLeuValGlnProGlnA 1057
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                                                                                                                                                                                                                                                                                                                 -----prothrthrPheLysProAsnSerProAspLeuAlaLys-----HisTyrLysS 941
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erAlaSerProGlnPro-AlaPheHisLeuLysProAspThrProVal-----SerVal
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959 LysLysHisHisVallleGlnGluLeuPrCLeuAspAsnThrPheValGlyGly-----
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IleValValIlePheValThrValLeuValArgCySArgHi8AlaSerArgPheLysAla
                                                    --- TGGAGCCCACCAGGCAAGAGGGGCCCAGCAGCCA
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LysLysLysArgLysArgLysSerProLysSerSerLeuLeuAsnPheValThr
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887 IleGlu--GluSerLysProAspAspAlaValHisGluProIleAsnĠlyThrIleSerL
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GTGATC------ATCACACTCCTCTTCATCTGTTGCCATTGCTGC
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Q8N3K7;
01-OCT-2002 (TrEMBLrel. 22,
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---GlySerGlnGluSerCysSerAspSerGlyLeuGlyAspHisGl 1038
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                                                                            KCOLS P.F.J., Van ROY F.;
KCOLS P.F.J., Van ROY F.;
"Identification and characterization of a novel human protocadherin
"Identification and characterization of a chromosome X-linked protocadherin.";
gene with high homology to a chromosome X-linked protocadherin.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                         GCAACCTGCTACAGTCCCCACCCTTGTGTCTTGATACAGACACACCAAG 1413
                                                                                                                                                                                                                                                                                                         ||| |||::: ||| ||| ||| span-CysTrpMetPro---ProGlyLeuGlyProTyrGlnHisProLys 1121
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PROSITE; PS50266; CADHERIN 2; 7.
Calcium; Calcium-binding; Call adhesion; Glycoprotein.
SEQUENCE 1203 AA; 132250 WW; CEEDD24FCICF8BE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hassy; F15118; Jacob PCDH9.

Genew, HGNC18661; PCDH9.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:call admin binding; IEA.

GO; GO:0007155; P:call admesion molecule activity; IEA.

GO; GO:0007155; P:call admesion; IEA.

GO; GO:0007156; P:homophilic cell admesion; IEA.

InterPro; IPR002126; Cadherin.

PERN; PR00208; cadherin; 6.

PRINTS; PR00205; CADHERIN.
                                                          TIGTGCAGGGAAGTACATTATCTACAGTCACAAAAATGTCT--
                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                  ----CATGGGAAAGCCTTGCCAGATTCAGACACATATA-
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Matches:
Conservative:
Mismatches:
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127.50
38.12%
22.93%
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1-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protocadherin-9.
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                                                                                                                                                                                                                                                                                        875 sCysProSerSerThrGlyPheHisIle-------GlnGluAsnGluGluSe 890
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                                                                                                                                                                                                                                                                                                                                                                                                                      910 ysSerAspSerGlyLeuGlyAspHisGluProValGlySerGlyThrLeulleSerHisP 930
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978 lnGluCysLeuValLeuGlyHisSerAspAsn-CysTrpMetPro---ProGlyLeuGly 996
                                                                                                                                                                                                                                                             1060 GTGTGCACATGCACGTAACACACACACACACAAATTCAGGTAGCAGGTACGTGGCAAGT
                      855 uHisThrArgdinCysAsnSerHisSerLysSerAspAsnlleProValThrProGlnLy
                                                                                                 --CysAspThrLeuSer-LysArgSerSerThrSerSerAspHi
                                                                                                                                                    930 roLeuProLeuValGlnProGlnAspGluPheTyrAspGlnAlaSerProAspLysArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of the Maria 420:563-573 (2002).

REMBL; AK029711; BAC26575.1; -.
MGD; MGI: A42105; 4910488P06Rix.
InterPro; IPR007086; ZIf_C2H2.
InterPro; IPR007086; ZIf_C2H2.sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            950 hrGluAlaAspGlyAsnSerAspProAsnSerAspGlyProLeuGlyProArg---
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                               937 CTATGTGTCCAATAGCAATGCTCCTTACTGCAGACCCAGGCATGCCTCC-----
                                                                                                                                                                                                                                                                                                                             1120 ATATICIGCICAICAAAIGGICAIIGGCIAIGIACITIGIGCAGGGAAGI----
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                                                                                                                              988 CCTGTCTCTGGCATACCCCACATGCAAAGCACAAAGAACATTT
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to zinc finger protein 37A.
                                                                                                                                                                                               1033 CCATACATCTCAATATGGTTCC-------
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ProTyrGlnHisProLys 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               778 TCTGACCACACACACATTTCAGGAACCCCTGAAATAATGCACTATGTCCATGTCCACA 837
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674 IleValValIlePheValThrValLeuValArgCySArgHiSAlaSerArgPheLysAla
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                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Calcīum; Calcium-binding; Cell adhesion; Glycoprotein.

1 1 1 NON TER
                                                                                                                                                                                Kochrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL834258; CAD38933.1; -.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0001559; F:calcium ion binding; IEA.

GO; GO:0007159; F:call adhesion molecule activity; IEA.

GO; GO:0007156; P:comphilic cell adhesion; IEA.

R GO; GO:0007156; P:comphilic cell adhesion; IEA.

R GO; GO:0007156; Cadherin.

R Ffam, PF00028; Cadherin.

R Ffam, PF00028; Cadherin.
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119180 MW; 89DBF082EF9E4373 CRC64;
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Last annotation update)
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                                     Hypothetical protein (Fragment).
DKFZP761B047.
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01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
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125.50
36.92%
22.05%
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                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                  TISSUE=Amygdala;
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     GTCACAAAAATGTCTCAT-
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ValproSerLeuSerAspProGlyThrGluAlaHisLeuCysGlyIleCysGlyLys---
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Pfam; PF00096; zf-CZHZ; 14.
PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf CZHZ; 4.
SWART; SM00355; Znf CZHZ; 14.
PROSITE; PS00028; ZINC FINGER CZHZ; 1; 13.
PROSITE; PS50157; ZINC FINGER CZHZ 1; 13.
SEQUENCE 468 AA; 52135 MW; 0C3AD98F4FZED7FD CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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GGGAAAGCCTTG 1211
                                                                                               CCAGATTCAGACACATATATACAATTTCCTAACCAGCAAGGCCCCCATACACCTTATT 1271
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Sciurognathi; Muridae; Murinae; Mus.
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STRAIM=ICR; TISSUB=Brain;
Goncalves N., Simon-Chazottes D., Creveaux I., Meiniel A.,
Gunent J-L., Meiniel R.,
Characterization, spatio-temporal expression and chromosomal assignment of mouse SCO-spondin.";
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257 ProTyralaCysSerAspCysGlyArgCysPheSerGluSerSerThr
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-GTTAGAAATAGGAAAGCATGCATCTGTAACCTGAGTGTTTATGG 1272
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                                                                          790 AsnCysThrAlaHisHisCysProArgGlnTrp-----AlaLeuCysProArgGlu 806
            ---CysValAlaGlyCysAsnCysProProGlyLeuLeuTrpAspLeuG 750
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| 962 GlyGlnAlaValThrValAsnGlyValSerIleArgLeuProLysValTyrThrGlyPro 981
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      BMBL, AJ491875. 2002 to the EMBL/GenBank/DDBJ databases.

BMBL, AJ491875. 20025541;

CO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005479; F:electron transporter activity; IEA.

GO; GO:0005179; F:electron transporter activity; IEA.

GO; GO:0005179; F:electron transport; IEA.

R GO; GO:0005179; F:electron transport; IEA.

R InterPro; IPR000203; BlueCu_1.

R InterPro; IPR000203; BlueCu_1.

R InterPro; IPR000203; BGF_like.

R InterPro; IPR000219; FASB_C.

R InterPro; IPR000219; TIL_Cvecptor_A.

R InterPro; IPR000219; TIL_Cverich.

R InterPro; IPR000884; TSPI.

R InterPro; IPR000884; TSPI.

R InterPro; IPR000884; TSPI.

R InterPro; IPR000884; TSPI.

R InterPro; IPR000895; VC_out.

R InterPro; IPR000895; VC_out.

R Pfam; PF00057; III_recept_a; 10.

R Pfam; PF00059; tspI.

R Pfam; PF00099; tspI.

R Pfam; PF00099; tspI.

R Pfam; PF00099; tspI.

R Pfam; PF00099; tspI.

R Pfam; PF00099; tspI.

R Pfam; PF00099; tspI.; 25.
to the EMBL/GenBank/DDBJ databases
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Matches:
Conservative:
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Indels:
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PROSITE; PS01186; EGF \(\frac{7}{2}\); 2.
PROSITE; PS00225; FASEQ 3; 1.
PROSITE; PS00261; GLYCC_HORMONE_BETA_1; 2.
PROSITE; PS00261; GLYCC_HORMONE_BETA_1; 2.
PROSITE; PS00268; LDLRA_1; 8.
PROSITE; PS00925; TS81; 25.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 2.
SEQUENCE 4998 AA; 535019 MW; DAZABA8DA.
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PROSITE; PS00196; COPPER BLUE; 1.

PROSITE; PS01225; CTCK 2; 2.

PROSITE; PS01026; EGF 2; 2.

PROSITE; PS0022; FASEC 3; 1.

PROSITE; PS00201; FASEC 3; 1.

PROSITE; PS00201; CALYCO HORNONE BET PROSITE; PS01209; LDLRA_1; 8.

PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00094; vwd; 3.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR01705; TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWART; SM00192; LDLa; 10.
SWART; SM00209; TSP1; 25.
SWART; SM00214; VWC; 4.
SWART; SM00215; VWD; 2.
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                                                                                                      euCysProGluProGlyAspLeuProHisProTrpAsnAlaHisArgAlaAsnTrpAlaP 1080
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0-107N-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
similar to zinc finger protein 135 (Clone pHZ-17) (Weakly similar 2inc finger protein 37A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| ::::|||||
|1140 isValArgTrpArgSerGlnGluLeuCysProLeuGlnCysGluGly-
                                                   --TGG--
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STRAIN=FVB/N; Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. [2]

[1] SEQUENCE FROM N.A. NCBI_TaxID=10090;

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19 lCysGlyLysSerPheGlnTyrSerAlaValLeuLeuArgH1sGlyArgAlaHisGlyGl 39
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    STRAIN=CS.7BL/6J; TISSUE=Embryo, and Lung;
STRAIN=22254683; PubMed=12466851;
The FANTOM Consortium.
The RANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:655-573(2002).
SEMEL; BC003258; AAH03258.1; -..
EMBL; BC03706; AAH3706.1; -..
EMBL; AK055113; BAC28948.1; -..
EMBL; AK055113; BAC39380.1; -..
EMBL; AK055166; BAC39380.1; -..
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MGD; MGI:2442105; 4930488P06Rik.

AGO; GO:0005634; C:nucleus; IEA.

InterPro; IPR007086; Znf_C2H2.

InterPro; IPR007086; Znf_C2H2.

Pfam; PF00096; zf-C2H2; I4.

R PRINTS; PR00048; Znf C2H2; I4.

R PROMOUN; PS00035; Znf CZH2; I4.

R PROSITE; PS00028; Znf CTHGER C2H2 1; I3.

R PROSITE; PS00028; Znf CFNGER C2H2 1; I3.

R PROSITE; PS0018; Znf CFNGER C2H2 2; I3.

R PROSITE; PS0018; Znf CFNGER C2H2 2; I3.

R PROSITE; PS0187; ZNC FNGER C2H2 2; I3.

R PROSITE; PS0187; ZNC FNGER C2H2 2; I3.

R PROSITE; PS0187; ZNC FNGER C2H2 2; I3.

R PCS PROSITE; PS0187; ZNC FNGER C2H2 2; I3.

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                       138 Phe-----ArgGlnSerAlaLeuProPheHisLeuAlaArgAlaHisProProGluIle 155
897 CAGGGACCACGIGGACAAIICIIGGAIACIGICIIGGCAGCIAIGIGICCAAIAGCAAIG 956
                                                               ----SerPheSerLysSerSerThrLeuThrArg 219
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                                                                                                                         174 ArgAlaPheHisSerSerAlaGlyLeuArgAsnHisSerArg-----IleHisVal
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363 -AsnHisAlaGlyHisLysProHisLysCys-----ProGluCysGlyLysSerPheSe
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                                                                                                                                              Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of mouse tensin 2.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424789; AAN32753.1; -
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                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGT:2387586; Tenc1.

GO; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR008973; C2 CalB.
InterPro; IPR006219; DAG PE-bind.
InterPro; IPR006020; PTB PID.
InterPro; IPR006020; ST2.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF0017; SH2; 1.
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SMART; SM00109; C1; 1.
SWART; SM00262; PTB; 1.
SWART; SM00252; SH2; 1.
SWART; SS0031; DAG PE BIND DOM 1; 1.
PROSITE; PS50031; DAG PE BIND_DOM_2; 1.
PROSITE; PS50001; SH2; 1.
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PRT;
                QBCJ95;
01-MAR-2003 (TrEMBLrel. 23,
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22.46%
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PRELIMINARY;
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                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                    | 11 | SECONDINCE FROM N.A. | 12 | SECONDINCE FROM N.A. | 13 | SECONDINCE FROM N.A. | 14 | STARIN-PUB/N; TISSUE-Salivary gland; STRAIN-PUB/N; TISSUE-Salivary gland; Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SECONDINCE | 15 | SE
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                                                                                                                                                                                                                                                                                  ---TATGATCTAGGAGGGGGGATCACCGGGATCCGGG 3007
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850 luSerProGluProSerTrpArgAspGlySerSerGlyHisSerThrLeuProArgSerP
                                                                                                                                                                                                                                                                                                                            870 roargaspProGlnCysSerAlaSerSerGluLeuSerGlyProSerThrProLeu----
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                                                                                                       --GCTGCCCTTCCTGTCTCCACCTCTC
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 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                           P SEQUENCE FROM N.A.

A GODENCE FROM N.A.

GODENOS., Creveaux I., Didier R., Meiniel R.;

"Characterization of cattle SCO-spondin.";

"Characterization of cattle SCO-spondin.";

"EMBL: AJ1348; Ca846239.1; -.

R HSSP; P56682; ACC.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005179; F:hormone activity; IEA.

R InterPro; IPR006208; Cys Knot.

R InterPro; IPR006208; Cys Knot.

R InterPro; IPR006209; Cys Knot.

R InterPro; IPR00639; TigP.1.

R InterPro; IPR00939; TigP.1.

R InterPro; IPR00939; TSP.1.

R InterPro; IPR00007; VWF.C.

Pfam; PF00007; Cys Knot; 1.

Pfam; PF00009; tsp1; 11.

R Pfam; PF00099; tsp1; 11.

R SMART; SM00068; GHB; 1.

R SMART; SM00209; TSP1; 11.

R SMART; SM00209; TSP1; 11.

R SMART; SM00209; TSP1; 11.

R PROSITE; PS00220; TSP1; 11.

R PROSITE; PS00220; TSP1; 11.

R PROSITE; PS00201; TSP1; 11.

R PROSITE; PS00201; TSP1; 11.
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Mismatches:
Indels:
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Matches:
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                                     Bovidae; Bovinae; Bos.
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                                                     AGTCCCCTAGAATGGATGGCTG---GGGAGGGTGGAGGCTGACAGCTGAGACGTAGTG 2968
                                                                                                     ---TATGATCTAGGAGGCGGATCACCGGGATCCGGG 3007
  -GCTGCCCTTCCTGTCTCCACCTCTC 2911
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                 3626 CAGAAAGACATCCCCTAGGCCTGGACTTCTGAGCAGCTTTAGCCAGGCTCCGGACGGCAG
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| luSerProGluProSerTrpArgAspGlySerSerGlyHisSerThrLeuProArgSerP
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01-NOV-1999 (TrEMBLrel. 12, La
01-JUN-2003 (TrEMBLrel. 24, La
SCO-spondin (Fragment).
SCO-SPONDIN.
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398 CysThrGlyGlyAlaAlaSerGlnGluArgProCysAsnLeuProSerCysThrGluLeu 417
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568 lylleValCysGlnGluAspGln-----AlaCysGlnGlnGlyCysArgCysProdluG 586
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01-JUN-2002 (TrEMBLrel. 21,
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372 TrpSerProCys-
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"Subcommissural organ/Reissner's fiber complex: characterization of SCO-spondin, a glycoprotein with potent activity on neurite outgrowth.";
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                 Meiniel A., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724C5FB8727E13DA CRC64;
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Mismatches:
Indels:
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Gila 32:177-191(2000).

EMBL, AJ416457; CAC94914.1, -.

GMG: GO:0005576; C:extracellular; IEA.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

InterPro; IPR006208; Cys knot.

InterPro; IPR006208; Cys knot.

InterPro; IPR006201; EA58 C.

InterPro; IPR006184; GIV hormoneB.

InterPro; IPR00184; GIV hormoneB.

InterPro; IPR00184; TSPI.

InterPro; IPR00184; TSPI.

InterPro; IPR00184; TSPI.

InterPro; IPR00184; WW D.

Pfam; PF00057; Cys knot; I.

Pfam; PF00057; Cys knot; I.

Pfam; PF00059; TSPI.10.

Pfam; PF00059; TSPI.10.

Pfam; PF00099; TSPI.10.

Pfam; PF00099; TSPI.10.

Pfam; PF00099; Vwd; 3.

PRINTS; RM00201; TSPSC; I.

SWART; SM00201; TSPI.25.

PROSITE; PS00225; TSPI.12.

PROSITE; PS00225; TSPI.12.

PROSITE; PS00225; CRYSTALIN BETAGAMMA; I.

PDOSITE; PS00225; CRYSTALIN BETAGAMMA; I.
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PROSITE; PS01286; FA58C 1; 1.
PROSITE; PS01286; FA58C 2; 1.
PROSITE; PS0022; PA58C 3; 1.
PROSITE; PS0022; PA58C 3; 1.
PROSITE; PS0020; DLKA 1; 7.
PROSITE; PS0109; LDLKA 1; 7.
PROSITE; PS50068; LDLRA 2; 9.
PROSITE; PS0109; TSP1; 25.
PROSITE; PS0109; WWFC 1; 1.
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MEDLINE=20465125; PubMed=11008217;
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TISSUE=Subcommissural organ;
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| Oy 229 ATCTCGGCCAGAACTGCTTTCCTGGAGGTCACGIACGIACGIACGIACGIACGIACGIACGIACGIACG | 169 | Db 4058MetGluValValSerCysAlaAsnArgCysProArgArgC, Qy 109 CACTCAGCTGTTTGAGTCTCAGGTTTCTTCATCTCCAAAAATG | 4077 | Oy 61 AATCTTTCGGTCCGCGGAAGGCCTTCCTG | Qy 25 AGGGAATCTCCTGG 12 4115 InGlyHisSerTrp 4119 | RESULT 15 Q7Z5J3 TO COPETS DEPLIMINARY. PRT: 451 AA. | 072533, 07-0CT-2003 (TEMBLrel. 25, Created) 01-0CT-2003 (TEMBLrel. 25, Last sequence 01-0CT-2003 (TEMBLrel. 25, Last annotati | BNF1. Homo sapiens Eukaryota; M | Mammalia; Eutheria; Primates; NCBI_TaxID=9606; [11] | RP SEQUENCE FROM N.A. RX PubMed=12853144; RA Wu I., Moses M.A.; RT "RMF-I. a novel gene encoding a putative extracellu | is overexpressed in tumor tissues."; Gene 311:105-110(2003). EMBL, AY163868; AAO31809.1; | SEQUENCE 451 AA; 49675 MW; CFBFUBFA7D5BCFE3 Cment Scores: | 113.50 | MISHACMES: Indels: Gaps: | US-10-776-827-10 (1-4460) x Q7Z5J3 (1-451) | Oy 318 GTGGCATGCCCAAAGCTGGAAGAGGAATAAATTACA | Qy 378 CTTTTGAGCTCAGGACCTGCTTGTAAGCCGAGAGGGTTC | 93 | Oy 423 CCTAATCTAGCCAACAC | | DD 120 GILLEGERIGERAGERAGERAGERAGERAGERAGERAGERAGERAGERA | 148 | Qy 528 GGGAGTCCTCCTGGGCCTGCCACTTTGGTGATCATCACAC |
|--|-----|---|--|-------------------------------------|---|---|--|---------------------------------------|---|---|--|---|--|--------------------------------|--|---|--|---|--|---|--|---|--|
| 1081 TGTGTTACGTGCATGTGCACACACCTTGGGAACCATATTGAGATGTATGGATAAATGTTCT 1022 | | | 982 GGCATGCCTGGGTCTGCAGTAAGGAGCATTGCTATTGGACACATAGCTGCCAAGACAGTA 923 | TCCAAGAATTGTCCACGT | | 3847 TrpAspLeuGluTyrCy8ProSerProGluCy8ProGlyAlaalaGlySerThrAlaGlu 3866 886 CCACTGGGACACTTAGTCTGGGGTTTGTTCCTTGGTTGAGTAGTTACTCTGTGGACA 830 | 3867 ProalaThrGlyLeuProGlyGlyTrpGlyLeuTrpSerPro 3880 829 TGGACATAGTGCATTATTTCAGGGGTTCCTGAAATGTCTGTGTGTG | ::: 3881 TrpSerProCys | | 709 TCTCCATCTGGAGAAAGCTTGGGTTGAGCAGAGATCCAGAGGTCTTCTTCATCCTTCTTCT 650 1890 AspProAlaHisProAlaTrpArgSerArgSerArgSerArgLeuCysLeuAlaAsn 3906 | 649 TCTTCTTCTTCTTCTTCT | | 3927 ProLeuCysProGlyProGlyCysGluAlaGlyAsnCysSerTrpThrAlaTrpAlaPro 3946 589AATGCAACAGATGAAGAGGAGTGTGATGATCACCAAGAGTGGCAGGC 542 | | 541 CCAGGAGGACTCCCAGGCAGATGGTGTTGTAGATGCCTTCTT 500 | 3967 ProproGlyProGlyGlyHisTrpCysProAspvalheUinfAlalyIsLinciunigArig 5500 499 | 3987 PhecysAsnieuArgAlaCysProValProdlyGlyTrpSerArgTrp 4002 | 469 AGCTGAAGACGCACTGATTCTCCATGGTCGCTTGGCTTG | CICGGCTIACAAGCAGGICCIGAGCICAAAAGGAIGCAACCIIGACCACIIGIAAIITAI | 4012 sGlyGlyGlyArgSerLeuArgSerArgSerKy8 4023 349 TCCTCTTCCAGCTTTGGGCATGCCACGTGACAGCACCTCCACACACA | ::: ::: | 289 ATGGCCAGCCAGCTTGGAGGAGCCTCCTTCCACGTTACTTCTTGCGTTGTCAGGG 230 | 4031 lyGlyAlaProCysValGlyGluArgHisHisAlaArgLeuCySAShFroinfrioCySG 4031 |
| ð | g ? | <u>2</u> 4 | δ f | 8 8 | 8 & | 음 & | qa OX | d : | g G | Oy Dp | ò á | a k | ag 8 | g 45 | δλ | ga <i>k</i> o | QQ | දු දු | ð | <u>අ</u> | ପୁ | 8 | đ |

CysGluCysThrAspAlaG 4115 |||| |GlyCysArgCysProGluG 4095 ||| | CysSerCysThrGluGlyGln 147 ATCTACAACCATCTGCCT 527 CTCCTCTTCATCTGTTGCCA 587 TCTCTGGC------ 422 roSerGlyLeuArgAlaPro 107 GAGAG----- 449 -----CAG 467 |||| |CysSerAspLeuGlnGluG 4077 |||||| |yGluIlePheSerAlaHis 127 rejererecijeggaaggr 110 229 ATCTCCGCCCAGAACTGCTTTCCTGGAGGTCACGTTCAACGTAGTAAACAATGGCTGAACA 170 'GGG------GAAC 62 ------CAGGCCC 26 lular matrix protein, a; Euteleostomi; RC64; 451 38 124 134 23 ò

| OY 580 OY 641 | |
|-------------------|--|
| | B TTGCTGCTGGAGCCCACCAGGCAGAGAGGCCAGCAGAGAAGAAGAAGA |
| Db 18 | 648 GAAGAAGAAGGATGAAGAAGACCTCTGGATCTCTGCTCAACCCCAAGCT 695 ::: |
| Qy 69 Db 20 | 96 |
| Oy 75 | 24 5 |
| Oy 81 Db 23 | 816 ATGCACTATGTCCATGTCCACAGAGTAACTACTCAACC |
| Qy 85 Db 24 | 858 AACAAACCTCAGACTAAGTGTCCCAGGGGACCCAGGGACCACGTGGACAATTC 917 |
| Qy 91. | 918 TIGGATACTGTCTTGGCAGCTATGTGTCCAATAGCAATGCTCCTTACTGCAGACCCA 974 |
| Qy 97: Db 289 | 75 GGCATGCCTCCCACCTGTCTCTGGCATACCCCACATGCAAAGGACAAA 1022 |
| Oy 102: | 023 GAACAT 1028 |
| 1 | TATCATACATCTCAATATGGTTCCCAAGTGTGCGCACATGCACGTAACACACAC |
| Qy 1089 Db 344 | ACAAATTCAGGTAGCAGGTAGGTGGCAAGTATATTCTGGCTCATCAAATGGTCATTGGCT ::: ::::::::::::::::::::::::::::: |
| Oy 1149 Db 357 | ATGTACTTTGTGCAGGGAAGTACATTATCTACAGTCACAAAAATGTCTCATGGGAAAGCC |
| Qy 1209 Db 372 | TTGCCAGATTCAGACACATATACAATTTCCTAACCAGCAAGGCCCCCATACA ::: |
| Oy 1263 Db 392 | |

Search completed: September 21, 2004, 15:40:58 Job time : 503 secs

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- mouse

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Trickly receptor beta chain precursor (ANA 11) - rabbit (5.8pecies: Oryctolagus cuniculus (domestic rabbit) (5.8pecies: Oryctolagus cuniculus (domestic rabbit) (5.8pecies: Oryctolagus cuniculus (domestic rabbit) (5.8pecies: Oryctolagus cuniculus (domestic rabbit) (5.8pecies: 30-Jun-1987 #sequence revision 30-Jun-1987 #sequence revision 30-Jun-1987 #sequence rayola (5.8pecies: 1.9pecies:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurocan precursor
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-MODBL=frame+ n2p.model-1DEV=xlp
-Q-/cgn12 1/USPTO_spool_p/US10776827/runat_21092004_133241_20790/app_query.fasta_1.4615
-Q-/cgn2 1/USPTO_spool_p/US10776827/runat_21092004_133241_20790/app_query.fasta_1.4615
-DB=PTR_78 -QFRT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=5its -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=5its -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-USER=US10776827_GCGN_1 1_221_Grunat_21092004_133241_20790 -NCPU=6 -ICPU=3
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-USER=US10776827_GCGN_SES=0 -MATRIX=0-SPELOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOF=10 -XGAPPEXT=0.5 -FGAPOP=6
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| % 92 | 993CTCTGGCATACCCCACATGCAAAGCACAAAGAACATTTATCCATACATCTCAATATG 1049 V ::: |
| δ | Н |
| qq | 64CysThrHisThrHisThrCys-ThrHisThrHisIleHis 76 |
| δō : | GIGGGCAAGIAIATICTGCTCAICAAAIGGTCAITGGCTAIGTACTITGIGCAGGAAGT |
| qq | 77AlaSerThrHisValCysIleHisThrHisThrPheThrHisLeuCysIl 93 |
| රු අු | 1170 ACATTATCTACAGTCAAAAAATGTCTCATGGGAAAGCCTTGCCAGATTCAGACACATAT 1229 |
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| λõ | 1290 ACAGATGCATGCTTTCCTATTTCTAACTCTAAACTTTTACTGGAAGTACTCATA 1349 |
| οp | 127 gGlnLeuSerAlaAlaLeuLeuLeuProThrProLeuHisPheProGluAspLeuAlaAs 147 |
| ά | 1350 ATTGGACATTCCAGCAACCTGCTACAGTC1378 |
| QQ | .:: 147 nValSerAlaPro-GinValValValPheAspProSerGluAlaGluIleAsnLysThrG 167 |
| ٥'n | 1379CCCACCCTTGTGTGTGTATACAGAC |
| QO | |
| ٥٨ | 1406ACACCAAGITTCTGTGCCTCTGACCTGTGCCAA 1445 |
| QQ | 187 rpTrpValAsnGlyLysGluValHisAsnGlyValSerThrAspProGlnProTyrLysG 207 |
| ò | 1446 GATGTTTAAAGTGTGATGGTTCAAAAATTCATTGAAAGCTCTTTTTCTT1492 |
| QQ | :: 207 lnAspProLysSerAspHisSerLysTyrCysLeuSerSerArgLeuArgValSerAlaA 227 |
| ò | 1493GTAACTCATGACAAAGTCCGTCCTCAT |
| Db | 227 laPheTrpHisAsnProArgAsnHisPheArgCysGlnValGlnPhePheGlyLeuT 246 |
| λŏ | 1545 TCCAAGACCTCTCTGTGAAACATTACCCCCGGAACCACTCAGCAAAGTGCCTTTCTCCA 1604 |
| QQ | 246 hrAspAspAspGluTrpThrTyrAsnSerSerLysProlleThr 260 |
| à | 1605 AGCAAGAACAAAGAGCTCTTGGTGGTGACTGCTAGAAAATTATGGAAGCCCACTCATTTA 1664 |
| qa | 261GlnAsnIleSerAlaHisThrArgG 269 |
| ٥x | 1665 IGTCAGTGGAACTGCAACTGTGTACCTGTGCAATGTTTACAGAAAGGGTGAAGGGTGAGGAGAT 1724 |
| Db | 269 lyArgAlaAspCysGly274 |
| δy | 1725 GCTACACCTGAGCTAGGTATCTCCTATATAACCAAAGGTTTCCAGCAGGAAGGA |
| ДD | 275 283 |
| ð | 1785 CAATCATCAGTGCAGTCTCACAGAAGGCAACACTG 1819 |
| Db | 284ValLeuSerAlaThrValLeuTyrGluIleLeuLeuGlyLysAlaThrLeu 300 |
| RESULT 2 | |

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R;Morch, M.D.; Boyer, J.C.; Haenni, A.L.

Nucleic Acids Res. 16, 6157-6173, 1988

A;Title: Overlapping open reading frames revealed by complete nucleotide sequencing of A;Reference number: S01955; MuID:88289359; PMID:3399388

A;Accession: S01955

A;Accession: S01955

A;Accession: S01955

A;Accession: S01955

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A;Cross-references: EMBL:X07441; NID:g62222; PIDN:CAA30321.1; PID:g62223

A;Cross-references: EMBL:X07441; NID:g62222; PIDN:CAA30321.1; PID:g62223

A;Note: the authors translated the codon ACG for residue 459 as U
C;Superfamily: hydroxyproline-rich glycoprotein
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175 aThrArgGlyProSerPheArgProIleLeuLeuProLysValValHisValHisAspAs 195
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|135 oSerArgPheProHisHisPheHisAlaArgArgProAspValLeuProSerValProAs
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oProArgProlleThrProGlyProSerAshThrHisAspLeuArgProLeuSerValLe 275

255

hypothetical protein, 69K - turnip yellow mosaic virus C;Species: turnip yellow mosaic virus, TYMV C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-2000 C;Accession: S01955

| & | 3276 TAACTAGAGGAGTÇÇÇAGTGCAGGATAGGCCCTAAACGTTTTGTTAATAAATAAACAGGTGCA 3335 | qq | |
|--------------------------|--|----------------|---|
| Db | | ò | 2859 CCACAACTGCCACTGCTC 2876 |
| ογ | 3336 IGAAAGGAGCCTAAGGCCATTGTTGATATCCACTCTTTTTCCACTTCCTTC | q _Q | 80 ProLeuHisProLeuValPheProGlyHisHisSerGlnLeuArgHisValHisGluThr 99 |
| qa | 291 sArgThrSerThr-GlyHis 297 | ò | 2877ACCAGACAAGCTGCCCTTCCTGTCTCCACTCCAGTCCCCCTAGAATGGATG 2930 |
| 'n | 3396 TITICICCARGITITAIGCITCICIGATICCCICTICIGCCIGCACAGACAGCC 3451 | qq | 100 GlnGlnValGlnGlnThrCysProGlyLysLeuLysLeuSer 113 |
| Db | 298 | ολ | 2931 GCTGGGGAGAGGTGGAGGCTGACAGCTGAGGTGTCGGGATATGATCTAGGAGGGCG 2990 |
| à | | qa | 114 |
| Dþ | 309 rofroserArgLeuGlnArgFro-ValHisLeuTyrGlnSer-SerFroHisThrProAs 328 | δλ | 2991 GATCACCGGGATCCGGGACCATACAAGTAACATGGTTTCCATGGCAACTGCTTG 3044 |
| à | 3510 TGGCAACCCATGGGACCAGACCAGAGACTGCTTGACTCATCTGGGG 3558 | Ор | 116 GluGluLeuProProAlaProGlnArgGlnHisSerLeuProLeuHis-IleThrArgPr 135 |
| qq | ArgL | ò | 3045 CTCG |
| δ | 3559 | Dp | 135 oSerArgPheProHisHisPheHisAlaArgArgProAspValLeuProSerValProAs 155 |
| Db | 347 yHisLeuGluArgLeuGlyGlnProAlaAsnLeuArgThrSerGluArgSerProPro 366 | δλ | 3073GTCATTGCCATGACAAGGCCTCTATCT 3099 |
| ò | 3585 ATGATTCCTAAAGAAGAGCTTCCTAGACCAGGCTCCAGAAAGACATCCCCTAGG 3644 | QQ | 155 pHisGlyProValLeuAlaGluThrLysProArgThrSerValArgGlnProArgSerAl 175 |
| Db | Argheu ProArgSerSerGluProAsnArgLeuPro | ζó | 3100CCAGGCACAAIGICCCIGCIGITCCIAAI3129 |
| δ | 3645 CCTGGACTTCTGAGCAGCTTTAGCCAGGCTCCGGACGGCCAGCCA | QQ | 175 aThrArgGlyProSerPheArgProlleLeuLeuProLysValValHisValHisAspAs 195 |
| Db | 383 ProLeuProGluAlaThrLeuAlaProSerTyrArgHisArgProTyrPro 400 | ò | 3130CCAATGGACTTGCTCTCACCCCAGGATGAAACACCCCAGAAACTCACT 3177 |
| ٥٧ | твстсстттссссаттестсаатва | QQ | |
| ΩÞ | ::: 401 LeuLeuProAsnProProAlaAlaLeuProSerIleAlaTyrThrSerSerArgGly 419 | δ | 3178TCTCAGTCACTTCCACGGGGGGGGGGGGGGGGGGG |
| ٥٧ | 3765 AGG 3767 | Ωp | 215 lArgArgProLeuLeuAlaProAsnGlnPheHisSerProArgGlnProProProLeuSe 235 |
| qq | 420 Lys 420 | δ, | 3204 TCAGAAGAGCCAAACCCAGAATGGGGCCTCTTTTC 3240 |
| RESULT 3 | | Ωp | : 235 rAspAspProGlyIleLeuGlyProArgProLeuAlaProAsnSerThrArgAspProPr 255 |
| SISISO hypotheti | . cal protein, 69K - turnip yellow mosaic virus | ò | 3241CCCATCACAGACTCCCCTGACAAC |
| C; Date: 2 | 7. curing fairor mosare views, inv. 7. Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000 60. 019150 | QΩ | 255 oProArgProlleThrProGlyProSerAsnThrHisGlyLeuArgProLeuSerValLe 275 |
| R; Dreher, | Oli olilista T.W.; Bransom, K.L. Bill 10 403-406 1002 | ò | 3276 TAACTAGAGGAGTCCCAGTGCAGGATAGGCCCTAAACGTTTTGTTAAATAAA |
| A; Title: | Franc. Mor. Broi. 19, 403-409, 1392. A;File: Genomic RNA sequence of turnip yellow mosaic virus isolate TYMC, a cDNA-based c b.Reference number. S19150. MITD.40119251. DMID.1731908 | QD | 275 uProArgAlaSerProArgArgGlyLeuLeuProAsnProArgArgHi 291 |
| A; Accessi | to manager. Signal, Morbington, Entring of the State of t | <i>λ</i> δ | 3336 IGAAAGGAGCCIAAGGCCAITGITGAIAICCACTCTCTTCTTTCCACTTCCTTC 3389 |
| A; Molecul | e type: geomic RNA :e type: geomic RNA :8: 1-628 < DRE | QQ | 291 sArgThrSerThrGlyHislieProProThrThrThrSerArgProThrGlyProProSe 311 |
| A, Cross-r C, Superfa | A;Cross-references: EMBL:X16378; NID:g62218; PIDN:CAA34414.1; PID:g62219 C;Superfamily: hydroxyproline-rich glycoprotein | හි 1 | rcatcititicicalgititalgciicicagaitaccicitagaacaaacaag |
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| ď | 2748 AICCCCTTGTCACATAGAGATTTGTCAIGGGGCCTCTGGCTGTGCCCTTC 2798 | දු දි | 35.2 |
| ΩD | 40 LeuproMetValHisSerGluGlyThrSerThrProThrGlnLeuLeuArgHisProAsn 59 | 3 8 | |
| δλ | 2799 ACATAACAGAATAACTIGCCATCTGCCTGCACCAAACCCAGGGATGTGGAAGACATCTCC 2858 | 3 | |

| 282 AlaMetAspThrTyrSerGlyProProGlyProMalateusSerBerboserLysValHisGly 319 618 | ACCATCACTGCCTGTTTAGTTAGGTGAGCAGAGGTGTTTCCTTTCTGGGGCTAAGCC ::: | |
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| Db 366 0ThrLysArgArgLeuProArgSerSerGluProAsnArgLeuPro 381 Qy 3642 AGGCCTGGACTTCTGAGCAGCTTTAGCCAGGCGCGCCAGCGAGGAGGCCTTTC 3701 ::: | RESULT 4 A36749 transcription factor HNF-1A - human NyAlernate names: hepatic nuclear factor 1-alpha; transcription factor 1, hepatic; tran C;Species: Howo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision for Inversection in Sacretary C;Date: 10-Sep-1999 C;Date: 10- | Alignment Scores: |

| 17 18 18 18 18 18 18 18 | | Oy 3457 CCTTTATTCCTCTCCATTTTCACTCCTTCC Db 435 LysLeuTrpSerArgAlaSerSerProPro Qy 3514 AACCCATGGGACCTCAGGACCAGAGAC Db 455 HisProGluGluAlaLeuArg | 2700 QY 3571 206 Db 462 2736 QY 3624 226 QY 3669 | 246 2823 251 2871 | | 314 334 3135 354 3183 |
|---|--|--|---|--|---------------|---|
| Db 595 LeuValler RESULT 5 JOHOLD A, Mote: 10-66K prote: C, Species: Ononis yell(A, Note: 10-28p-1990 #sc C, Accession: JOHON R, Ding, S.W.; Keese, P A, Fittle: Nucleotide see A, Fattle: Nucleotide see A, Reference number: JOHON A, Accession: JOHON A, Accession: JOHON A, Accession: JOHON A, Residues: 1-597 cDIN A, Cross-references: GB Alignment Scores: Perent Similarity: Dercent Similarity: Dercent Similarity: COURTY MATCh: Db 187 ProLysPr COY 2701 Db 207 ProCysAr; COY 2701 Db 277 Db 277 COY 277 COY 2764 GAGAGTT DD 277 ACGAGG | ical 66K protein - Ononis yellow mosaic virus s: Ononis yellow mosaic virus s: Ononis yellow mosaic virus s: Ononis yellow mosaic virus of yellow mosaic virus of yellow mosaic virus of yellow mosaic virus of yesp-1990 #text_change 08-Oct-100: J00107 seep-1990 #text_change 08-Oct-1102, 555-563, 1989 Nucleotide sequence of the ononis yellow mosaic tymovirus genom nee number: J00106; MUID:90021186; PMID:2800337 ion: J00107 for yellow mosaic tymovirus genom ion: J00107 for yellow mosaic tymovirus genom for J00107 for yellow mosaic tymovirus genom reference: GB:J04375; NID:q332572; PIDN:AAA46795.1; PID:q332573 | cores: 0.189 Length: 112.00 Matches: Conservative: 33.25% Conservative: Similarity: 22.64% Mismatches: 1.40% Indels: 2 | -10 (1-4460) x JQ0107 (1-597) CCTCTCACCCTATATGGCCATAAACTGCCTAA | ProLeuProSerSerLysProLeuSerLeuGl. GACAGTTTGTCATGGGGCCTCTGGCTGTGCCC | , a a a c a a | CysSer valArg valArg coldinger GACTTG |

| 8 6 8 6 8 6 8 6 8 6 8 | 375 3232 394 3292 3397 3397 432 3457 3457 3457 3514 455 3514 3514 3514 3514 | • | a 3 TTCCC 3 TTCCC 3 TTCCC 3 GAGC 3 GACC 3 GACC 3 TTCA 3 TTCA 3 TTCA 3 TTCA 3 TTAGC 3 | 393 3291 396 3345 3346 413 3456 434 454 454 451 3623 3668 490 |
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| a % a % a | 414 3397 432 432 435 3514 3571 3624 462 369 | | 4 6 4 6 4 6 4 6 4 6 4 6 4 | 131 134 134 1513 1570 161 162 175 175 175 |
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| qq | 3624 476 3669 | | ω 4 м п | \$668 \$90 3728 |
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| q | 3669 | | | 3728 |
| δō | | | ::: prepret | |
| qa | 491 | | 61WIIII | 506 |
| δλ | 3729 | | | |
| qa | 507 | ::: TrpvalGlnCys 510 | | |
| RESULT 6 T45746 hypothetic C,Species: C,Date: 0C,Accessic R,Vitale, Submitted A,Referenc A,Accesside A | ARESULT 6 TA5746 hypothetical pro (1,5pecies: Arabic (2,0pecies: Arabic (2,0pecies: Arabic (2,0pecies: Arabic (3,0pecies: Arabic (3,0pecies: Arabic (4,0pecies: Arabi | tein F24M12.190 - Arabidop dopsis thaliana (mouse-ear 000 #sequence_revision 04-746 #sequence_Database er: Z23012 #sequence Database er: Z23012 #sexury DNA es: EMBL:AL132980 ource: cultivar Columbia; 399/1; 132/3; 170/3; 198/1 90 | aext_change 04-Feb-2000 De Simone, V.; Mewes, H 1999 24M12 2/3; 284/2; 396/3; 441/ 968 99 74 1150 1150 | H.W.; Lemcke, |

| 10 CORGANCOGANGGATOSTICCCONTITUDGGATORACGANGACTCANGCAGCTCANGCAGCT 100 CORGANCOGANGAGATICCCONTITUDGGATORACGAGACTCCANGCAGT 110 CORGANCOGANGAGATORACGAGACTCCANGCAGT 110 CORGANCOCANGCAGAGACTCCANGCAGACACTCCANGCAGACACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACACTCCANGCAGACACTCCANGCAGACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACTCCANGCAGACACACACTCCANGCAGACACACACACACACACACACACACACACACAC | 684 ArgSerCysGlyAlaSerPheValSerSerSerSerIeuSerGluArgAspAla 953 AArGCCCCTACTGC | Db 762 MetlleLysSerSerProAsnGlySerGlnValSerThrSerLysSer 777 Qy 1088 CACAAATTCAGGTAGGTAGGTGGGCAA 1117 | :92 on; | Son (1-352) CARCCAAGCTTCCCAGATGGAG |
|--|---|---|---|--------------------------------------|
| | GCGGACCGAAAGGATGTTCCCCATTTGGAGAAACTGAGACTCAAAGCGGCTGA ::: :::: | | yalaserserProAlaGinHisLeuAlaPheValThrProAspGlnSerArgValGl TGGAGGAATCAGTTCTTCAGCTCTATCTGGACACCATCTTGACCAA TGGAGCAATCAGTTCTTCAGCTCTATCTGGACACCATCTTGACCAA nGlyGluArgLeu | |

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| Percent Similarity: 30.57* Conservative: 37 Best Local Similarity: 22.07* Mismatches: 155 Query Match: 1.33* Indels: 147 DB: 2 Gaps: 17 | US-10-776-827-10 (1-4460) x JQ0110 (1-628) | 0 1 | D O | 27 | 60 IleTrpPheGlyAsnileProProProProArgArgProGinAspAsnArgAset | 2859 CCACAACTGCCACTGCTCACCAGGACAACTICCLICLICLICCLACCICCACCICACCAC | CAGCTGAGACGTAGTGTCAGATA | 92 | 2976 TGATCTAGGAGGGGGGGATCACCGGGATCCGGGACCATACAAGTAACATGGTTTCCATGGC ::: | Db 9595 | | euProProAlaProGl | Oy 3058 -AGACAGTCAGTTGTCATTGCCATGACAAGGCCTCTATCTCCAGGCACAATGTC 3113 | | TGAAACACCCAGAAACT :: PYONS | sAlaArgArgProAspValLeuProSerLeuProAspHisGly | æ | 159 lLeualaGluThrLysProArgThrSerValArgGinProArgSeFilnrinrArgGivFr 1/ | 3231 CTCTTTCCCCATCACA | | | en . | 209 gGinbeuGinProintileArgArightGriobeumeum.cr.com.com.com.com.com.com.com.com.com.com | 3379CCACTTCCTTCTCTTTITICCTTTATAGETTAGETTAGGETTAGGAGG | 229 GGINFIOFIODEUGELSEFASFASFIOCATATAGOCAT | 3429 CTTCTGCCTGCACCAGCCCCAGCCTTATICCLLCATITITICS | 249 snSerThrArgAspProPro-ProArgProlleThrProGlyFroFneAshillraise17 | OY 3483 ILCMACLICISTOCTO ::: ILCMACLICISTOCTO | נסא נ | ArgArgHisArgThr | Qy 3525 CCTCAGGACCAGAGACTGCTTGACTCATCTGGGGAGGTAAGTTCACGGGGGAC 3578 |
|---|--|-----|------------|----|---|--|-------------------------|----|--|---|-----|------------------|---|--------------------------------------|----------------------------------|--|---|--|-------------------------|--|------|------|--|--|--|---|--|---|--|--|--|
| QY 930 TIGGCAGCTAIGTGCCAAIAGCAAIGCTCCTTACTGCAGACCCAGGCAIGCCTCCCACC 989 | UB /9 | 79 | 1050 GITCC | 08 | QY 1110 GTGGGCAAGTATATTCTGCTCATCAAATGGTCATTGGCTATGTACTTTGTGCAGGGAAGT 1169 | | SACACATAT | 94 | Qy 1230 ATACAATTTCCTAACCAGGCACCCCCAIACACCALIGATICCALAACCACTCAGGGGGAAGGCCCCCCAIACACCALIGATICCALAACCACTCAGGGGAAGGCCCCCCAIACACCALIGATICCALAACCACTCAGGGAAGGGGAAGGGGAAGGGGAAGGGAA | 1290 ACAGATGCATGCTTTCCTATTTCTACCTCTACACATAAACTTTTACTGGAAGTACT | 121 | 1350 ATTG | 138 | OV 13711374CTACAGTCCCACCTTGTGTC 1394 | | Qy 1395 TTGATACAGACACACCAAGTTTCTGTGCCTCTGAGCCCTCACGAGAGGTGTTTAA 1454 | Db 178 LeuCysGlyCysTyrSerValSerValLeu-ProGlyCysAlaGluProTrpAs 196 | D- | SysThrAlaAlaTyrProGluSe | Oy 1515 CTCATTGCCACTGAGGGTGTTTAATGTGATCCAAGACCTCTCTGTGA 1562 | 1563 | | RESULT 8 | OVOLLO hypothetical 69K protein - turnip yellow mosaic virus C. Species: turnip yellow mosaic virus, TYMV | C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 19-May-2000 C.Date: 07-Sep-1900 #text_change 19-May-2000 | C; Accession: uquilu R; Keese, P.; MacKenzie, A.; Gibbs, A. H: A. A. A. A. A. A. A. A. A. A. A. A. A. | Virology 172, 536-546, 1589 A,Title: Nucleotide sequence of the genome of an Australian isolate of turnip yellow mos A,Title: Nucleotide sequence of the genome of A:Reference number: J00109; MIID:90021184; PMID:2800335 | | A;Residues: 1.628 <kee> A;Cross-references: GB:J04373; NID:g332244; PIDN:AAA46591.1; PID:g332245</kee> | A;Experimental source: Australian isolate C;Superfamily: hydroxyproline-rich glycoprotein | Alignment Scores: 0.55 Length: 628 Pred. No.: 107.00 Matches: 96 |

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Wed Sep 22

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A,Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t
A,Reference number: PQ0328, MUID:92198477, PMID:1550588
                                                                                                                                                                                                                                                        D.; Jones, C.; Forstner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2824 CCTGCACCAAACCCAGGGATGTGGAAGACATCTCCCCACAAATGCCACTGCTCACCAGGA 2883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ThrSerSerProLeuThrGluSerThrThrLeu------LeuSerThr 2081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProProAlaileGluMetThrSerThrAlaProProSerThrProThrAlaProThr
                     C.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: glycoprotein, intestine, tandem repeat
2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                  Basbaum,
                                        J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481; PMID:1985113
A;Accession: A61257
                                                                                                                                                                                                                                                     D.; Wang,
                P.S.; Gum, J.R.; Kim, Y.S.;
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                                                                                                                                                                                                                                                R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool,
Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                         A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 'T', 1925-1948, 'TTS', 1952-1954 cJAN> A;Experimental source: bronchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 2328-2468 <XUG>
A;Cross-references: GB:M86523
A;Experimental source: small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3064 CAGTCAGTTGTCATTGCCATGACA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 2328-2342,'K',2344-2354
                Yan,
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107.00
36.54%
26.92%
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                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                       A; Accession: PQ0328
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Cyptes 10-War-1393 Resequence revision 12-Apr-1996 #text_change 05-Nov-1999
Rydone 17. (18.; #HCKB. J.W.; Torblara, N.W.; Siddkik, B.; Kim, Y.S.
Tytes 10-War-1393 Resequence revision 12-Apr-1996 #text_change 05-Nov-1999
Rydone 17. (18.; #HCKB. J.W.; Torblara, N.W.; Siddkik, B.; Kim, Y.S.
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                                                                                              PheArgProSerGlyIleArgLysAspAlaPheLeuGlnThrGlyProArgLeuGlyHis 348
ProProSerArgLeuGlnArgProValHisLeuHisGlnSerGlyProHisThrProAsp 328
                                                                                                                                                                                       349 LeuGluArgLeuGlyGlnSerAlaAspLeuArgThrSerGluArgThrProSerThrLys 368
                                                                                                                                                                                                                                                                                                                                                                                                                     LeualaProSerTyrArgHisArgArgSerHisProLeuLeuProAsnProProAlaAla 408
                                                                                                                                                                                                                                                                                                         :::
369 ArgArgLeuProArgProSerGluProAsnCysLeuProSerSerLeuProGluAlaThr
                                                   3579 AAAAAATGATTCCTAAAGAAGAGGCTTCCTAGACCAGCACAGGCTCCAGA
                                                                                                                                                                  --AAGACATCCCCTAGG
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---LeuProProlleAlaTyrThrSerGlyArgGlyLys 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mucin 2 precursor, intestinal - human (fragments)
N;Alternate names: mucin SMUC-41
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Date: 10-Mar-1993 #sequence
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can result in familial adenomatous polyposis or sporadic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||
GluLeuSerProValAlaArgGlnThrSerGlnIleGlyGlySerSerLysAlaProSer
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2351 ProSerThrAlaSerThrLysSerSerGlySerGlyLysMetSerTyrThrSerProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LeuLysThrProAlaSerLysSer
A,Map position: 5q21-5q22
A,Note: mutations of this gene can result in familial adenomatous polynote: mutations of this gene can result in familial adenomatous polyposis cali protein C,Superfamily: adenomatous polyposis; tumor suppressor F;1-720,Domain: leucine-rich AMTD-F;1-720,Domain: leucine-rich AMTD-F;1-720,Domain: leucine-rich AMTD-F;1-721,Megion: coil #status predicted F;185-227/Region: coil #status predicted F;185-227/Region: acidic F;1131-1156/Region: acidic F;11866-1893/Region: acidic F;1866-1893/Region: highly charged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GGAGGGGGGATC---
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Mismatches:
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Matches:
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DB:
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A; Residues: 1-2843 «KIN»
A; Cross-references: GB: M74088; NID: g182396; PIDN: AAA03586.1; PID: g182397
A; Cross-references: GB: M74088; NID: g182396; PIDN: AAA03586.1; PID: g182397
A; Josylyn, G; Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grarington, J.; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Cell 66, 601-613, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenomatous polyposis coli protein - human

Althermate names: polyposis coli locus protein DP2.5; tumor suppressor APC

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 21-Ju1-2000

C;Accession: A37261; B39658; A44928; A449319; I54271

C;Accession: A37261; B39658; A44928; L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.;

R;Kinzler, K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.;

Science 253, 661-665; 1991

A;Title: Identification of FAP locus genes from chromosome 5q21.

A;Reference number: A37261; MUID:91335210; PMID:1651562

A;Accession: A37261.
                                                                                                                                                                                       3420
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                                                                                                                                                                                                                                                                                             3421 GATICCCICITCIGCCIGCACCAGACCAGCCCCAGCCCTITATICCTCTCCATTITCACT 3480
                                                                            -----AGGIGCAIGAAAGGAGCCIAAGGCCAI---IGIIG 3360
                                                                                                                                                                                                                                                                                                                                                                                                        CCTTCCAGCCTCTGTCCCTGAACTGCCACGCAACCCATGGGACCTCAGGACCAGGAG 3538
                                                                                                                                                                                                                                                                                                                                                                                                                                          elleArgThrThrGlyLeuArgProTyrProSerSerValLeuIleCysCysValLeuAs
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                                                                                                                               2180 nAspIhrTyrTyrAlaProGlyGluGluValTyrAsnGlyThrTyrGlyAspThrCysTy
                                                                                                                                                                                    3361 ATATCCACTCTTCTTTCCACTTCCTTCTCTTTTTCTCCATGTTTTATGCTTCTCT
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A;Molecule type: mRNA
A;Residues: 1-4 <LAM>
                                                                                                                                                                                                                                             rPheValAsnCysSerLeuSerCysThrLeu------
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A;Cross-references: GDB:119682; OMIM:175100
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| Oy 561 CATCACACTCCTTCATCTGTTGCCATTGCTGAGGCCCACCAGGCAAGAGGG | Qy 618CCAGCAGCCAGAGAAAAAAAAAAAAAAAAAAAA | Qy 666 AGACCTCTGGATCTCTGCTCAACCCAAGCTTCTCCAGATGGACAAGGACCCCCAGATGGACAAGGACCCCCAGATGGACAAGGACAAGGACAAGGACAAGGACAAGGACAAGAAG | Qy 717 ATCACTGCCTGTTTAGTTAGGCAGGAGGTGTTTCCTTTCTGGGGCTAAGCCTCC ::::: | Db 370ValSerAlaThrGlyGlyProLeuProProValSerThrLeu Qy 825 GTCCATGTCCACAGGGTAACTACTCAACCAAGGAACAAACCTCAGACTAAGTGCCCAGT | Qy 885 GGAGGGAGTCCCAGGGACCACGTGGACAATTCTTGGATACTGTCTTGGCAGCT | Qy 945 CCAATAGCAATGCTCCTTACTGCAGGCATGCCTCCCACTGTCTCTGGCATACC ::: ::: | liver- Qy 1005 CCACATGCAAAGCACAAAAAACATTATCCATACATCTCAATATGGTTCCCAAGTGTGTG | Qy 1065 CACATGCACGTAACACACACACACAAAATTCAGGTAGGTA | 1125 | OY 1185 ACAAAATGTCTCATGGGAAAGCCTTGCCAGATTCAGACACATATATACAATTTCCTAAC | Qy 1245 CAGCAAGGCCCCCATACACCATCTATACAACACTCAGGTTACAGATGCA | Qy 1299 TGCTTTCCTAFTTCTAACTCTACACATATAACTGGAAGTACTCATAATTGGACAT | Oy 1359 TCCAGCAACCTGCTACAGTCCCCACCCTTGTGTGTCTTGATACAGACACACCAAGTTTCT | Oy 1419 G 1419 Db 518 u 518 | RESULT 12 G01763 atrophin-1 - human C.Specides: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998 C.Accession: G01763 |
|--|--|--|---|--|--|---|--|---|---|---|---|---|--|----------------------------------|--|
| AGCCCC 345 | AGCCCTTATTCCTCTCATTTCACTCCTTCCAGCCTCTGTCCCTGAACTGCCACTGC | OINTATSSEIGLAALAGANTNIPPROVALLeuSerProSerLeuProAspMet: AACCCATGGGACC 3526 ::: ThirHisserSer 2498 | RESULT 11 A46149 transcription factor HNF-1A - hamster N;Alternate names: hepatic nuclear factor 1-alpha; transcription factor LF-B1 C;Species: Cricetinae gen. sp. (hamster) | C;Accession: A46149 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A46149 #sequence_revision 10-Sep-1999 C;Accession: A46149 | tion | Experimental Source: HIT-TIS M.2.2.2 insulinoma cell line Note: sequence extracted from NCBI backbone (NCBIP:110643) Complex: homodimer; can also form heterodimers with, for example, HNF-1B Function: | ression of a number of play other roles Y btion regulation | Region: dimerization 77/Domain: homeobox homology <hox> nt Scores;</hox> | Pred. No.: 0.841 Length: 630 Score: 105.00 Matches: 98 Percent Similarity: 33.97% Conservative: 45 Best Local Similarity: 23.28% Mismatches: 161 Query Match: 1.31% Indels: 177 | | 3ATCCCTGACAACGCAAA ::: LeuProThrLysLys | GCTGGAA rLvsGlu | GTTGCATCCTTTTGAGCTCAGGACCTGCTTGTAAG | AAGCACCATGGAGAATCAGTGCCTTCTT ::: | CACCATCITGACCAAACACCAAGAAGGCAICITACAACACCATCIG :::::::::::::::::::::::::::::::::::: |

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CCCTGAAATAATGCCACTATGTCCATGTCCACAGAGTAACTACTCAACCAAGGAACAAACC 865
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419 ------ValSerAsnGlnProProLysTyrTh 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ACTGCAGACCC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 TCTTCATCTG-----TTGCCTGCT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 oGlyHisLeuProSerProHisAlaMetGlyGlnGlyIleGlyGlyLeuPro---- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| ::::::||||||| || |----ProGlyProGluLysGlyProThrLeuAlaProSerProHisSerLeuProProAl 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GATCTCTGCTC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 aSerSerAlaProAlaProProMetArgPheProTyrSerSerSerSerSerSerSer
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                                                                                                                                                                                                                                                                                                                                             ----TCAGTGCCTTCTTCAGCTCTATCT 475
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                                                                                                                                                                                                                                                                                              -----TTCTCTGGCCCTAAT
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1153
A,Accession: G01763
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Acsierreferences: EMBL:U23851; NID:g915325; PID:g915326
C,Genetics: EMBL:U23851; NID:g915325; PID:g915326
A,Gross-references: GDB:DRPLA; B37
A,Gross-references: GDB:270336; OMIM:125370
A,Map position: 12p-12p
                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                              GGGACACCATCTTGACCAAACA-----
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Query Match:
DB:
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Score:
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|---|--|---|--|---|---|--|--|
| | ò | 974 | AGGCATGC | ŭ | TGTCTCTGG | TGTCTCTGGCATACCCCACATGCAAAGCA | 1018 |
| | Db | 458 | oGlyProPhel | ProProSerThrGly | oGlyProPheProProSerThrGlyAlaGlnSerThrAla | | 478 |
| | δλ | 1019 | CAAAGAACAT | TTATCCATACATCTC | AATATGGTTCCCAAG | CAAAGAACATTTATCCATACATCTCAATATGGTTCCCAAGTGTGTGCACATGCACGTAAC | 1078 |
| | qq | 478 | BHisHisHis | 1 | nglnglnglngln | -Hisglnglnglnglnglnglnglnglnglnglnglngl | 495 |
| | ò | 1079 | ACACACACACAAATTCA | ACAAATTCAGGTAG(| aggtacgtgggcaag | GGTAGCAGGTACGTGGCAAGTATATTCTGCTCATCAAATG | |
| | qq | 495 | nGlnHisHis(| GlyAsnSerGlyPro | proProProdiýAla | nglnHisHisGlyAsnSerGlyProProProProGlyAlaPheProHisProLeuGluGl | 515 |
| | ò | 1139 | GTCATTGGCTATGTAC | | -TTTGTGCAGGGAAGT ::: | -TTTGTGCAGGGAAGTACATTATCTACAGTCACAAA | 11 |
| | qq | 515 | yGlySerSer | ні зні вАІ ані вРтс | oTyrAlaMetSerPro | yGlySerSerHisHisAlaHisProTyrAlaMetSerProSerLeuGlySerLeuArgPr | Ŋ |
| | λ i | 1190 | AATGTCTCATGGGAAAGCC- | 1 2 | GCCAGATTCAGACACA | -TIGCCAGATICAGACACAIATATACAAITICCIAACCA | 1246 554 |
| | gg | 535 | oTyrProPro | GIYProAlaHisher | olyrbrogroglybroalamisheukrokrokromissergillivalserity. | GINVALSELLYL SELGI | , - |
| | දුරු ජි | 1247 | | CATACACCATCTAT: ::: AsnGlyPro | rccaraaacacrcaa | GCAAGGCCCCATACACATCTATTCCATAAACCACTTAGATTACAATTACAATAAAAAAAA | 561 |
| | οy | 1307 | TATTTCTAAC | TATTICIAACTCTACACATAA | ACTTTTACTGGAA | GGAAGTACTCA | 1347 |
| | Ωþ | 561 | ovalSerSer | :::::: SerSerAsnSerSe | | aSe. | 581 |
| | δλ | 1348 | | TAATTGGACATTCCAGCAACCT | | | 1369 |
| | qq | 581 | | SerGinGlyProGl | nGlyAlaProTyrPrc | SproSerProSerGlnGlyProGlnGlyAlaProTyrProPheProProValProThrVa | 601 |
| | λõ | 1370 | | GCTACAGTCCC | GCTACAGTCCCCACCCTTGTGTGTCTTGATACAGACACAC | GATACAGACACACCAAGT | 1414 |
| | qa | 601 | | SerAlaThrLeuSe | rThrvalileAlaTh | IThrThrSerSerAlaThrLeuSerThrValIleAlaThrValAlaSerSerProAlaGl | 621 |
| | ολ | 1415 | - | TTCTGTGCCTCTGACCCTCACCTGTGCCA | ACCTGTGCCA 1444 | | |
| | Db | 621 | | yTyrLysThrAlaSerProProGlyProProPri | yProProPro 632 | | |
| | SULT 1 Specie Cin JU Specie Access Addest Access Status Residu Cross- Cros- Cross- Cro | JULIO - JULIO | 3. 11.0 - human (fragme is: Homo mapiens (ma 06-Jan-1995 #sequention: 337595; 335048 id. to the EMBL Data ance number: 337593 iton: 337595 iton: 337595 iton: 337595 iton: 337595 iton: 337595 iton: 337595 iton: 337595 iton: 337595 iton: 339-337, id. to Porchet, N. J. 293, 329-337, id. to Degenerate 87-base since number: 335047 iton: 335048 it | gment) uence_rev 048 048 048 i.x 74956; N.; Audie ', 1993 asse-pair 147; MUID: 103.50 20.00% | 995 1DN: cre cre ::791 | #text_change 08-Oct-1999 CAA52911.1; PID:g407053 uperat, V.; Laine, A.; van- ate hydrophilic/hydrophobic 6618 330 67 67 114 | 9. van-Seuningen. obic alternat: |
| _ | DB: | | | 7 | Gaps: | 10 | |

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968 AGACCCAGGCAIGCCICCCACCIGICITCIGGCAIACCCCACAIGCAAAGCACAAAGAACA 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                1148 TATGTACTTTGTGCAGGGAAGTACATTATCTACAGTCACAAAAATGTCTCATGGGAAAGC 1207
                                                                                                                                                                                                                                                                          1208 CTTGCCAGATTCAGACACATATATACAATTTCCTAACCAGCAAGGCCCCCATACACCATC 1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1484 TCTTTTCTTGTAACTCATGACAAAGTCCGTCCTCATTGCCACTGAGAGGTGTTTAATGTG 1543
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                                          907
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-----ProGlnProArgLeuHisSerTyrProLeuLeuGlnProArgAspGlyThrHi 218
                                                                                                                                                24 TrplleLeuThrGluLeuThrThrAlaAlaThrThrThrAlaAlaThrAlaAlaThrAlaAlaThrAlaProHisCys 43
                                                                               23
                                                                                                                                                                                                                                                                                                                   -ThrAlaSerSe 76
                                                                                                                                                                                                                                                                                                                                                                                                94
                                      848 TCAACCAAGGAACAAACCTCAGACTAAGTGTCCCAGTGGAGGGCAGTCCCAAGGGACCACG
                                                                           5 ThrThrThrArgAlaThrSerSer---MetSerThrProSerSerThrProGlyMetThr
                                                                                                                 908 TGGACAATTCTTGGATACTGTCTTGGCAGCTATGTGTCCAATAGCAATGCTCCTTACTGC
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44 -AspProValLeuHisProArgAspHisLeuAspProHisArgAlaGlnHisTyrSerTh
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                                                                                                                                                                                                                                                                                                      63 rValThrValProThrGlySerGlnPro-
US-10-776-827-10 (1-4460) x S37595 (1-330)
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Ig alpha-1 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-May-1981 #sequence_revision 03-Oct-1995 #text_change 20-Oct-2000 C;Accession: A22360; A92249; Ā91662; S38979; B53110; A02171 R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H. Cell 36, 681-688, 1984 and Convergence of the human immunoglobulin alpha-1 and A;Reference number: A94653; MUID:84130179; PMID:6421489 A;Reference number: A22360 A;Molecule type: DNA A;Residues: 1-353 <FLA> FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Residues: 1-353 <FLA> A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79151016; PMID:107164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Reference number: A92249; MUID:79164 A;Refe
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A; Molecule type: protein

A; Molecule type: protein

A; Residues: 1-16, 27, 18, 18, 20, 18, 22-34, 07, 36-45, 27, 47-51, 18, 53-56, 12B, 59-61, 18, 6

303, 18, 305-346, 07, 348-353 ePUT>

A; Note: this is the final paper in a series

A; Note: this is the final paper in a series

A; Note: amidation states of residues 118, 197, 238, 239, 243, 244, 287, and 318 were ta

R; Kratzin, H.; Altevogt, P.; Ruban, E.; Kortt, A.; Staroscik, K.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 356, 1337-1342, 1975

A; Title: The primary structure of a monoclonal iga-immunoglobulin (iga Tro.), II: the ar

A; Reference number: A91662; MUID: 76023781; PMID: 809331
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A; Residues: 1-16, 72, 18, 18, 20, 18, 22-34, 0, 36-45, 21, 47-51, 18, 53-56, 2B, 59-61, 18, 6
A; Residues: 1-16, 72, 18, 18, 20, 245-283, 0, 20, 285-289, 18, 291-303, 18, 305-353 KRA>
A; Experimental source: myeloma protein Tro
B; Rallgreen-Gebauer, E.; Gebauer, W.; Bastian, A.; Kratzin, H.D.; Eiffert, H.; Zimmerman
Biol. Chem. Hoppe-Seyler 374, 1023-1028, 1993
A; Title: The covalent linkage of secretory component to IgA. Structure of sIgA.
A; Reference number: S38978; MUID: 94121784; PMID: 8292260
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A; Residues: 188-196, D', 199-201 < FAL>
A; Residues: 188-196, D', 199-201 < FAL>
A; Residues: 188-196, D', 199-201 < FAL>
B; Yang, C.Y.; Kratzin, H.; Gotz, H.; Hilschmann, N.
Boppe-Seyler's Z. Physiol. Chem. 360, 1919-1940, 1979
A; Title: Die Primaerstruktur eines monoklonalen IgAl-Immunglobulins (Myelomprotein Tro)
A; Reference number: A31644; MUID: 80114124; PMID: 393607
A; Contents: annotation; Tro, disulfide bonds
A; Note: Cys-14 bonds to a light chain
A; Note: Cys-14 bonds to a light chain
B; Calero, M.; Bscribano, J.; Grubb, A.; Mendez, B.
A; Title: Location of a novel type of interpolypeptide chain linkage in the human protein
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A;Reference number: A53110; MUID:94103241; PMID:7506257
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C; Complex: An immunoglobulin hear subunit consists of two identical light (kapper famin disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology (Keywords: chromoprotein; duplication; glycoprotein; heterotetramer; immunoglobulin homology (Keywords: chromoprotein; duplication; glycoprotein; heterotetramer; immunoglobulin homology (MD)
F; 243-315/Domain: immunoglobulin homology (MD)
F; 246-85.77-101,123-180,147-204,250-313/Disulfide bonds: #status experimental
F; 105,111,113,119,121/Binding site: carbohydrate (Ser) (covalent) #status experimental
F; 192/Disulfide bonds: interchain (to secretory component) (partial) #status experimental
F; 192/Disulfide bonds: interchain (partial) #status experimental
F; 192/Disulfide bonds: interchain (partial) #status experimental
F; 322/Disulfide bonds: interchain (partial) #status experimental
F; 322/Disulfide bonds: interchain (partial) #status experimental
F; 322/Disulfide bonds: interchain (partial) #status experimental
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A,Cross-references: GDB:119332; OMIM:146900
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A; Residues: 346-351,'X',353 <CAL>
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| Alignment Pred. No. | nt Scores: o.: | 1.18 | | | λ̈ | 1509 TC |
|------------------------------|--|--------------------------------|--|-----------|----------------------|--|
| Score: Percent | Similarity: | 103.00 27.64% | (9 | | qq | 209 0G |
| Best Local S Query Match: | Best Local Similarity: Query Match: | 21.65% 1.28% | Mismatches: 89 Indels: 165 | | ò | 1557 CT |
| DB: | | ~ | Gaps: 16 | | අු | 229 uV |
| US-10-776-827 | -10 (1 | -4460) x AlHU (1-353) | 53) | | RESULT | 15 |
| δ | 669 CCTCTGGA | TCTCTGCTCAACCCA | CTTCTCCAGATGGAG | 3T 728 | T46500 hvpoth | stical pro |
| Db | 10 ProLeuSe | ProLeuSerLeuCysSerThrGln- | | /s 26 | C;Spec | C;Species: Homo C:Date: 04-Feb-2 |
| λŏ | 729 TTAGTTAG | TTAGTTAGGCAGGAAGCAGAGGTGTTTCCT | JITTCCTGGGCTAA | AA 770 | C; Acce | ssion: T46 |
| ΩÞ | ::: 27 LeuValGln | | GlyPhePheProGlnGluProLeuSerValThrTrpSerGlu | lu 43 | R;Otte submit | waelder, sed to the |
| 'n | 771 GCC | | -TCCTTCTGACCACACACACATTTCAGGAACCCCT | E 809 | A; Acce | ssion: T46 |
| qa | 44 SerGlyGl | nGlyValThrAlaAr | ::: SerGlyGlnGlyValThrAlaArgAsnPheProProSerGlnAspAlaSerGlyAsp | 62 | A; Mole | cule type: |
| ò | 810 GAAATAAT | GCACTATGTCCATGT | GAAATAATGCACTATGTCCATGTCCACAGAGTAACTACTCAACCAAGGAACAAACTCAG | AG 869 | A; Expe | A; Cross-referenc A; Experimental s |
| qq | | | -LeuTyrThrThrSerSerGlnLeuThrLeuProAl | | C;Gene A;Note | cics: : DKFZp434 |
| ΟŸ | 870 ACTAAGTG | STCCCAGTGGAGGGCA | actaagtgtcccagtggagggaggcccagggaccacgtggacaattcttggatactgtc ::: ::: | | Alignment | ent Scores |
| С | 75 ThrGlnCy | ThrGlnCysLeuAlaGly | | 80 | Pred. No.: Score: | Q |
| ò | 930 TTGGCAGC | TATGTGTCCAATAGC | TTGGCAGCTATGTGTCCAATAGCAATGCTCCTTACTGCAGACCCAGGCATGCCTCCCACC | CC 989 | Percent Best Loc | Percent Similari Best Local Simil |
| qa | 80 | | | 80 | Query DB: | Query Match: |
| δλ | 990 TGTCTCTG | 3GCATACCCCACATGC. | TGTCTCTGGCATACCCCACATGCAAAGCACAAAGAACATTTATCCATACATCTCAATATG | TG 1049 | US-10- | US-10-776-827-10 |
| QQ | 80 | | | 80 | 2 | 2650 43 |
| δ | 1050 GTTCCCAA | AGTGTGCACATGCA | GTTCCCAAGTGTGCACATGCACGTAACACACACACACACA | AC 1109 | 3 | M |
| Db | 81Ly | sservalThrCysHi | | 92 | } | 2710 A |
| ζ | 1110 GTGGGCAA | AGTATATTCTGCTCAT | GTGGGCAAGTATATTCTGCTCATCAAATGGTCATTGGCTATGTACTTTGTGCAGGGAAGT | GT 1169 | 7 A | 29 V8 |
| qq | 92 | | | 92 | l è | |
| À, | 1170 ACATTATO | CTACAGTCACAAAAT | ACAITAICTACAGICACAAAAAIGICTCAIGGGAAAGCCIIGCCAGAIICAGACACAIAI | AT 1229 | 3 6 | |
| qq | 93 | | ProSerGlnAspValThr | hr 98 | 3 8 | 2824 (2) |
| λ | 1230 ATACAATI | TTCCTAACCAGCAAGG | ATACAATTTCCTAACCAGGAAGGCCCCCCATACACACCATTTCCATAAACCA | -ACT 1283 | 3 E | |
| Ωp | ::: 99 ValProC ₃ | ysProValProSerTh | ::: ValbroCysProValProSerThrProProThrProSerProSerThrProProThr | hr 117 | ò | |
| δλ | 1284 CAGGTTAG | CAGATGCATGCTTTCC | CAGGITACAGAIGCAIGCITICCIAITICIAACICIACACADAACITITACIGGAAGIA | TA 1343 | : A | 72 S |
| Ор | 118 ProSerP | ProSerProSerCysCysHisPro- | oArgLeuSerLeuHisArgProAlaLeuGluAsp | sp 136 | ò | 2929 T(|
| λŏ | 1344 CTCATAA | CTCATAATTGGACATTCCAGCAACCTG | CCTG | 1370 | - 원 | 84 - |
| qa | 137 LeuLeuL | eudlyserGluAlaAs | LeuLeuLeuglySerGluAlaAshLeuThrCysThrLeuThrGlyLeuArgAspAlaSer | er 156 | ò | 2983 - |
| È | 1371 | | CTACAGTCCCCACCCTTG | TG 1388 | 7 A | 93 G |
| qq | 157 GlyValT | hrPheThrTrpThrPi | oSerSerGlyLysSerAlaValGlnGlyProPro | 31u 176 | ò | 3037 A |
| δλ | 1389 TGTGTCT | TGATACAGACACACC! | TGTGTCTTGATACAGACCACCAGGTTTCTGTGCCTCTGACCCCTCACCTGTGCCAAGAT | 3AT 1448 | qa | 113 8 |
| СD | 177 ArgAspL | euCysGlyCysTyrSe | ArgAspLeuCysGlyCysTyrSerValSerSerValLeu-ProGlyCysAlaGluPr | 195 | ò | 3097 T |
| δ | 1449 GTTTAAA | GTGTGATGGTTCAAA | GITIAAAGIGIGAIGGIICAAAAIICAIIGAAAGCICIIIIICIIGIAACICAIGACAAAG | AAG 1508 | qa | 121 S |
| đ | 195 oTrpAsn | | HisGlyLysThrPheThrCysThrAlaAlaTy1 | CPr 209 | | |

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ACTGCTTGCTCGTTTGAATTAAGACAGCAGTCAGTTGTCATTGCCATGACAAGGCCTCTA 3096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-------CCAGGCACAATGTCCCTGCTGTCTCCTAATCCAATGGACTTGCTC 3144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GGAGGGGGGATCCGGGACCATACAAGTAACATGGTTTCCATGGCA 3036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTIGCCCTCTCACCCTATATGGCCATAAACTGCCTAAGCACTCAGGCCTCCCACTCATC 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARCCCTITICACCAGAGAAGAAGCACTCTGGTTCTCTATCCCCTTGTCACATAGAGAGT 2769
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CCGTCCTCATTGCCACTGAGGGGTGTTTAATGTGATCCA------AGACCTCT 1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5500 B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. ne Protein Sequence Database, January 2000 ber: 223031
                                                                                                                                                                                     otein DKFZp434D098.1 - human (fragment)
.sapiens (man)
2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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valThrTyrSerTyr-------GlyGlyAlaValProSerTyr-----
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149 cAAA.
169 : BMBL:AL137564
source: adult testis; clone DKFZp434D098
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Mismatches:
Indels:
Gaps:
                                                                          TGTGAAACATTACCCCCGCAAACCACTCAG 1587
                                                                                                  ValHisLeuLeuProProProSerGluGlu 239
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Matches:
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|SerAlaGluSerLeuGlu-------
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Search completed: September 21, 2004, 15:44:56 Job time : 197 secs Human Human

Abp96069 Abu54581 Abg04954 Aab68080

Amino Human

Aay99382 | Aab66131 Aau29164 |

Aau02749 Aab48069

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Sequence:

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Abr74983 | Abr94745 | Abu85718 | Abu98878 |

Human

Abu91799 Abu89492

Abu98093

Human

Abu96269 Abu92700 Abo08777 Abo02829

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Human; angiogenesis; cytokine; cell proliferation; pluripotent; cell differentiation; cotipotent; stem cell; transplantation; bio-sensor; neuroepithelial cell; autoimmune disease; neural cell; genetic disorder; nerve; brain tissue; central nervous system disease; peripheral nervous system disease; peripheral nervous system disease; neuropathy; haematopoiesis; bone; myeloid disorder; lymphoid cell disorder; platelet disorder; tendon; regeneration; cartilage; tendon; ligament; nerve tissue growth; tissue repair; wound healing; burn; ulcer; osteoporosis; cancer; osteoartritis; bone degenerative disorder; periodontal disease; gut protection; lung fibrosis; liver fibrosis; reperfusion injury; immune deficiency; infection; autoimmune disorder; heroditary disorder; biochythm; circadian cycle; fertility; metabolism; catabolism; anabolism; nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic, vulnerary, antiulcer, osteopathic, antiarthritic, vasotropic, immunostimulant, antibacterial, fungicide, immunosuppressive,
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                                                                                                                Homo sapiens.
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              ABO00556;
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Command line parameters:
-MODEL=frame+.n2b.model -DEV=xlp
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-LOOPEXT=0 -UNITS=bits -TARN=-1-RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15
-USER=US10776827_@CGN_1_1_651_@runat_21092004_133239_20757_-NCPU=6 -ICPU=3
-NO MMAP -LARGEOUERY -NORS=0 -MATRIX=0 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aboo0556 Novel hum
Aam49810 Human KIA
Aam49809 Human KIA
Aa057525 Human col
Aa011854 Human pol
Abo00836 Polypepti
Abul1838 Human MDD
Aau08755 Human ins
Abg01683 Novel hum
Aag80596 Human cad
                                                                                                                                     September 21, 2004, 15:03:24 ; Search time 374.5 Seconds (without alignments) 6729.836 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                              1 cggggcagcaaccaggagat......aattaaaggtatactagctc 4460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                               using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
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AAO11854
ABO00836
ABU1838
AAU1838
AAU08753
AAG80596
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                                                                                                                                                                                                                                                                                                        BLOSUMO.
Xgapop 10.0 , Xgapext ,
Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext halop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqn19908:*
geneseqp20008:*
geneseqp20018:*
geneseqp20028:*
geneseqp20038:*
geneseqp2003bs:*
geneseqp2003bs:*
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geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                 - protein search,
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                                                                                                   nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jatabase :
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4 5 6 5 6 5 1

Result

13-SEP-2002; 2002WO-US029001.

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Comprehensive invention relates to the isolation of novel mean persent invention relates to the isolation to novel mean polymeticle exception relates to an enable to any objectides exhibit activities relating to angiogenesis, cytokine, cell polymeticles exhibit activities relating to angiogenesis, cytokine, cell principal activities. The polypeptides are involved in the proliferation, differentiation and survival of pluripotent and totipotent of proliferation, differentiation, maniferature of bio-phasmaceuticals and the calls, and are useful for re-engineering damaged or diseased tissues, transplantation, maniferature of bio-phasmaceuticals and evelopment of bio-sensors. The polypeptides can be used to manipulate stem calls in culture to give rise to neuroepithalal cells that can be used to augment or replace calls damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptides and brain tissue and are useful for the treatment of central and peripheral nervous system and are useful for the treatment of central and peripheral nervous system of proliferation of neuropathies, such as Altahamer's, Parkinson's disease, anyonived in chemotractic or chemokines system of proliferation of haematopoiesis and are useful for treatment of central and peripheral and peripheral conformation of haematopoiesis and are useful for treatment of the central and peripheral and disease. The polypeptides are also useful for gut protection of regeneration and treatment of lung or liver fibrosis, reperitation and erreatment of lung or liver fibrosis, repetitation of periodontal disease. The polypeptides are also useful for growth, in various tissues, various immune deficiencies and disorders infections, such as asthma or other respiratory problems. The polypeptides are involved in thrombolysis or thrombolysis and are useful in thrombolysis or thrombolysis and are useful for any activity, and are useful for treating activity and are useful for treating activity and are useful for treating activity and are
                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides for diagnosis, treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 479; 300pp; English.
                                        13-SEP-2001; 2001US-0322511P.
12-SEP-2002; 2002US-00243552.
                                                                                                                                                   Yang Y, Wang Z,
                                                                                                                                                                                           2003-313249/30.
                                                                                                                                                                                                                                                                                                                           lateral sclerosis.
                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                               N-PSDB; ACD05633
                                                                                                                                                   Tang YT,
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9900 R H Matches: Conservative: Mismatches: Indels: 2.18e-43 507.50 96.97% 96.97% 6.32% Best Local Similarity: Sequence 99 AA; Percent Similarity: Alignment Scores: Query Match:

ftp.wipo.int/pub/published_pct_sequences

41 ilenhrieurenpheileCysCysHisCysCysTrpSerProProGlyLysArgGlyGln 60 673 TGGATCTCTGCTCAACCCAAGCTTCTCCAGATGGAGAAGAGACCATCACTGCTTT 729 1 MetGluArglleSerAlaPhePheSerSerlleTrpAspThr1leLeuThrLysKisGln 21 GluGlyIleTyrAsnThrIleCysLeuGlyValLeuLeuGlyLeuProLeuLeuValIle 562 ATCACACTCCTTTCATCTGTTGCCATTGCTGGAGCCCCACCAGGCAAGAAGAGGGCCAG 502 GAAGGCATCTACAACACCATCTGCCTGGGAGTCCTCCTGGGCCTGCCACTCTTGGTGATC 81 Trp11eSerAlaGlnProLysLeuLeuGlnMetGluLysArgProSerLeuProVal US-10-776-827-10 (1-4460) x ABO00556 (1-99) g g 8 g à à 엄 ò

Ma Y;

Weng G,

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RESULT 2

AAM49810 standard; protein; 47 AA AAM49810

AAM49810;

(first entry) 16-JUL-2002

Human KIAA0040 neo cMNR region #2.

MSI+; microsatellite instability tumour cell; neopeptide; cMNR; cDNR; mononuclectide microsatellite; gene therapy; diagnosis; tumour; human; dinuclectide microsatellite; cytostatic; immunisation.

Homo sapiens

WO200204664-A2.

17-JAN-2002.

04-JUL-2001; 2001WO-DE002510.

07-JUL-2000; 2000DE-01032608.

(DOEB/) KNEBEL DOEBERITZ M.

Gebert J, Yuan YP, Bork P, Doeberitz M, Linnebacher M; Knebel

WPI; 2002-171723/22.

Mutant genes isolated from tumors showing microsatellite instability, useful for diagnosis, treatment and prevention of tumors, also related peptides and antibodies.

Claim 3; Fig 2; 31pp; German.

This invention describes novel genes isolated from MSI+ (microsatellite instability) tumour cells, containing coding mononucleotide or dinucleotide microsatellites (cMNR and cDNR), differing by mutations in centra or corresponding genes of non-MSI+ (tumour) cells, and encoding 'neopeptide'-containing gene products. The products of the invention have cytostatic activity, are capable of inducing a specific immune response (humoral and cellular) and are useful for gene therapy. The products of the invention are used for the molecular investigation and diagnosis of MSI+ tumors (or their precursors) and are useful for prophylactic or therapeutic immunisation against MSI+ tumors. This sequence represents the human KIAA0040 neo cMNR region described in the disclosure of the invention

Sequence 47 AA;

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CCTTGCCAGATTCAGACACATATATACAATTTCCTAACCAGCAAGGCCCCCATACACCAT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                   CTATTCCATAAACCACTCAGGTTACAGATGCATGCTTTCCTATTTCTAACTCTACACATA 1326
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human;
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                                                                                                                                                                                                                                                                                                                                 ProCysGlnIleGlnThrHisIleTyrAsnPheLeuThrSerLysAlaProlleHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LeuPheHisLysProLeuArgLeuGlnMetHisAlaPheLeuPheLeuThrLeuHisIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSI+; microsatellite instability tumour cell; neopeptide; cMNR; mononucleotide microsatellite; gene therapy; diagnosis; tumour; dinucleotide microsatellite; cytostatic; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Woerner
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                                                                                                                                                                                                                                    (1-47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTITIACTGGAAGTACTCA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human KIAA0040 neo cMNR region #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM49809 standard; protein; 49 AA.
                                                                                                                                                                                                                                    US-10-776-827-10 (1-4460) x AAM49810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knebel Doeberitz M, Bork P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUL-2001; 2001WO-DE002510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000; 2000DE-01032608
                      .89e-18
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                                               267.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-171723/22
                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200204664-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Alignment Scores:
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1119 TATATTCTGCTCATCAAATGGTCATTGGCTATGTACTTTGTGCAGGGAAGTACATTATCT 1178
                                                                                                                                                                                    GTGCACATGCAC---GTAACACACACACACACACAAATTCAGGTAGCAGGTACGTGGGCAAG 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and variety and can be used in gene therapy and treatment of diseases associated with inappropriate P expression. For example, N and P may be used in the prevention, diagnosis example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorcatal
                                                                                                                                                                                                     1 ValHisMetHisValThr-HisThrHisThrGlnIleGlnValAlaGlyThrTrpAlaSe 20
                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                 20 rllePheCysSerSerAsnGlyHisTrpLeuCysThrLeuCysArgGluValHisTyrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                          440
77017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein SEQ ID NO:6489.
                                                                         Conservative:
                                                                                        Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA;
                                                         Matches:
                                                                                                                                                                                                                                                                                                               1179 ACAGTCACAAAATGTCTCATGGGAAAG 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 7965-7966; 9803pp; English.
                                          Length:
                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                              US-10-776-827-10 (1-4460) x AAM49809 (1-49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colorectal carcinoma; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                           AAG75725 standard; protein; 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                            1.3e-16
                                                       249.50
94.00%
94.00%
3.11%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-235357/24.
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                           Alignment Scores:
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                                            Pred. No.:
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Tang YT,
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                                                                                                                                         Query Match:
                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                         RESULT
                                                                                                          Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. agges 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                             2844 GTGGAAGACTTCCCCCACAACTGCCACTCACCAGGACAAGCTGCCCTTCCTGTCTC
                                                                                                                                                                                                                        CACCTCTCAGTCCCCCTAGAATGGATGGCTGG-GGAGGTGGAGGCTGACAGC 2956
                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 25746; 1399pp + Sequence Listing; English.
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11
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                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 25746.
                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                             AA011854 standard; protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US004927
                                                                                                                   170.00
97.37%
94.74%
2.12%
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                            Similarity:
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                                                                       Sequence 88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                  AA011854;
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                                                                                                                                                                                                                                                          2904
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                                                                                                                                                     Query Match:
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Human, anglogenesis, cytokine, cell proliferation; pluripotent;

cell differentiation; totipotent; stem cell; transplantation; bio-sensor;

cell differentiation; totipotent; stem cell; transplantation; bio-sensor;

meuroepithelial cell; autoimmune disease; neural cell; genetic disorder;

merve; brain tissue; central nervous system disease;

peripheral nervous system disease; neuropathy; haematopoiesis; bone;

myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;

tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;

tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;

tissue architis; bone degenerative disorder; periodontal disease;

yut protection; lung fibrosis; liver fibrosis; reperfusion injury;

immune deficiency; infection; autoimmune disorder; allergic reaction;

kw hrombolysis; thrombosis; coagulation disorder; hereditary disorder;

notropic; neuroprotective; antiparkinsonian; anticonvulsant;

notropic; uneuroprotective; antiparkinsonian; antiarthritic;

vasotropic; immunostimulant; antiasthmatic; ottostatic; virucide.
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treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ProHisThrAspIleSerGlyThrProGlulleMetHisTyrValHisValHisArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACACACACATTTCAGGAACCCCTGAAATAATGCACTATGTCCATGTCCACAGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides for diagnosis, treatment of and peripheral nervous system diseases and neuropathies, such as
                                                                                                                                                                                                                                000088
                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                           (1-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTACTCAACCAAGGAACAAACCT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrThrGlnProArgAsnLysPro 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO00836 standard; protein; 28
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2002US-00243552.
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                                                                                                                                                                                                                          2.68e-07
159.00
100.00%
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                                                                                                                                                                                                                                                                                                                                       1.98%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-313249/30.
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                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACD05913.
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                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2003
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                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                  Sequence 28
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The present invention relates to the isolation of novel human polynoleocide sequences and their encoding polyspeptides. The novel polynoleocide sequences and their encoding polyspeptides. The novel polynoleocide sequences and their encoding polyspeptides. The novel polypeptides are involved in the prolypeptides are involved in the growth factor activities. The polypeptides are involved in the prolypeptides and are useful for the engineering damaged or diseased tisseased transplantation, ammifacture of bio-pharmaceuticals and development of bio-sensors. The polypeptides are used to manipulate stem cells in culture to give rise to neuroepithelal cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptides induce the can be used to augment or restment of central and peripheral nervous system diseases and neuropathelas, such as Alzheimer's. Parkinson's disease, and neuropathelas, such as Alzheimer's. Parkinson's disease, and neuropathelas and requencation of harmatopoids and are useful for treating myeloid or lupphoid cell disorders. In chemication of harmatopoids and are useful for treating myeloid or regeneration of bone, cartilage, tendon, ligament and/or nerve tissue for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, in tissue repair. The polypeptides are also useful for gut protection or respencation and treatment of lung or liver fibrosis, reperfusion induving severe combined immunodeficiency (SCID), bacterial or fungal including severe combined immunodeficiency (SCID), bacterial or fungal including severe combined immunodeficiency (SCID), allergic reactions and continued arthritis, disbetes mellitus, myasthenia gravis), allergic reactions and continued sorders (including hereditary disorders and involved in thrombolysis or thrombosis and are useful in the cameer. They also inhibit the growth, infection or function of infections cancer. They also inhibit the growth, infection are involved ande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded by novel contigs assembled in the examples of the present
invention. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                          Example 3; SEQ ID NO 960; 300pp; English
                             lateral sclerosis.
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000088 Conservative: Mismatches: Indels: Matches: 68e-07 159.00 100.00% 100.00% 1.98% Similarity: Sequence 28 AA; Percent Similarity: Alignment Scores: Query Match: Best Local

US-10-776-827-10 (1-4460) x ABO00836 (1-28)

783 CCACACACACATTTCAGGAACCCCTGAAATAATGCACTATGTCCATGTCCACAGAGTA 842 1 ProHisThrAspIleSerGlyThrProGlulleMetHisTyrValHisValHisArgVal ACTACTCAACCAAGGAACAAACCT 866 843 21 셤 ò ò

20

RESULT 7
ABU11838
ID ABU1

ABU11838 standard; protein; 1213 AA.

cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia; anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic; antipsoriatic; hepatotropic; gene therapy, protein replacement therapy, cell proliferative disorder; MDDT; human; disease detection and treatment molecule polypeptide; Human MDDT polypeptide SEQ ID 785. 29-MAR-2001; 2001US-0280067P. 29-MAR-2001; 2001US-0280068P. 16-MAY-2001; 2001US-0291280P. 17-MAY-2001; 2001US-0291849P. 17-MAY-2001; 2001US-0299428P. 20-JUN-2001; 2001US-0299428P. 20-JUN-2001; 2001US-0299476P. 27-MAR-2002; 2002WO-US009944. (first entry) psoriasis; hepatitis. WO200279449-A2 Homo sapiens. 28-MAR-2001; 13-FEB-2003 10-OCT-2002. ABU11838;

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME; Daffour GE, Hilimon.
Daugherty SC, Dam TC,
TC, David MH, Daugherty SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R, Daffo A,

(INCY-) INCYTE GENOMICS INC.

WPI; 2003-058431/05. N-PSDB; ABX34828 New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.

Claim 27; SEQ ID NO 785; 339pp + Sequence Listing; English.

This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-iHIV, haemostatic, nephrotropic, ortostatic, anti-HIV, haemostatic, nephrotropic, antipsoriatic and hepatotropic activity. The polymucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, releasemia, lymphoma, melanoma, myeloma or sarcoma, anaemia, Crohn's leukaemia, lymphoma, melanoma, myeloma or sarcoma, namemia, Crohn's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis, ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Etp.wipo.int/pub/published_pct_sequences

Sequence 1213 AA;

Alignment Scores:

1213

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:::::: :::||||||||||||||----GlyLeuAlaGluAlaThrGluMetCysThrGlnGluCysLeuValLeuGlyHisS 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated insulin-like growth factor binding protein-like (IGFBP-like) polypeptides and their associated polymuclectides. The DNA sequences can be detected by contacting a sample with nucleic acid primers that anneal to the DNA and amplifying a product comprising a portion of the sequence. Detection of the product indicates the presence of DNA. The protein sequences can be detected by contacting a sample with a compound that binds to the polypeptide to form a complex. Detection of the complex indicates the presence of the protein. The sequences of the invention are useful for treating a subject having a need to inhibit activity or expression of IGFBP-like sequences. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involves administering an antagonist of the polypeptide, a polymerotide that inhibits the expression of the mucleotide sequence or a therapeutic amount of the polypeptide that competes for its ligand and a carrier. The sequences are useful in treatment of disorders such as cancer, or to
                                                                                                                                                                                                                                                                                                Insulin-like growth factor binding protein, IGFBP; human; cancer; lemale reproduction; embryo development; food supplement; gene mapping; medical imaging; autoimmune disease; nervous system disease; cytostatic; cerebrovascular disease; wound healing; gynaecological; antiinfertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promote female reproductive health and embryo development. They can also be used in food supplements, in medical imaging and in gene mapping. The sequences can be used in the treatment and prevention of autoimmune diseases, nervous system diseases, cerebrovascular diseases and infertility and for enhancing wound healing. This sequence represents a human IGFBP-like polypeptide
                                                                                                                                                                                                                                                                 Human insulin-like growth factor binding protein-like polypeptide #2.
                                                                         New insulin-like growth factor binding protein-like polypeptide and encoding polymucleotides, useful for treating cancer, infertility, arthritis, and for increasing wound healing.
                                                    CCAGCAACCTGCTACAGTCCCCACCCTTGTGTGTCTTGATACAGACACACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YT;
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23-AUG-2000; 2000US-00649167.
14-FEB-2001; 2001US-00784748.
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897 IleGlu--GluSerLysProAspAspAlaValHisGluProlleAsnGlyThrlleSerL
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352 ysAlaLeuProThrTyrSerTyrSerSerThrLeuSerProSer 366
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193 luGluGluGluGluGluGluGluGluGluGluLysGluGluGluGluGlyCysLysSerA 213
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
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Sequence 572
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                    GGCCATTTTGCTGCTGTGTGTGGAGGTGCTGTCAGTGGCATGCCCAAACCCAAAGCTGGA 343
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87 ProGlyLeu-ValCysAlaSerGlnAlaAlaGlyAlaAlaAlaProGluGlyThrGlyLeuCy 106
                                                                                                          CATCCTTTTGAGCTCAGGACCTGCTAGTAAGCCGAGGGGTTCTCTGTGGCCCTAATCTAGC 433
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193 luGluGluGluGluGluGluGluGlyGluGluGluGluGluGluGluGlyCysLysSerA
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233 heGlnProSerMetlleAspIlelleAspGluAlaSerThrLeuHisValAlaGlnHisA
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                                           GiyalaGluGlyAlaSerCysGlyGlyArgAlaGlyGly
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 US-10-776-827-10 (1-4460) x ABG01683 (1-390)
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222 IleGlu--GluSerLysProAspAspAlaValHisGluProlleAsnGlyThrIleSerL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human cadherin 63 polypeptide and its encoding polynucleotide. The invention also discloses a method for production of the polypeptide. The product of the invention can be used for the treatment of various diseases, such as malignant tumours, haemolysis, HIV infection, immunological diseases and inflammations. Thi sequence represents the human cadherin 63 described in the method of the
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142 TyrGlnAsnGluAspTyrLeuThrIleMetIleAlaIleIleAlaGlyAlaMetValVal
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                                                                                                 Human, cadherin 63, malignant tumou:
immunological disease, inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                               (BODA-) BODAO GENE TECH CO LTD
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                                                         ----ProThrThrPheLysProAsnSerProAspLeuAlaLys-----HisTyrLysS
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sectivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LeuGinileGinAlaArgLys 182
                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involving aberrant protein expression or biological activity. The bolypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                              Claim 20; SEQ ID NO 55594; 103pp; English
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958 TCCTTACTGCAGACCCAGGCATGCCTCCCACTGTCTCTGGCATACCCCACATGCAAAGC 1017
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                                                                                 roalaThrProHisAspProArgThrThrProAspHisProSerHisIleLysProHisA 251
                                                                                                                                         251 laProThrAsnGlnGlnProAspThrLeuThrProThrHisHisHisThrAspThrA 271
                      CTCCTCTTCATCTGTTGCCATTGCTGCTGGAGCCCACCAGGCCAAGAGGGGCCAGCAGCA
                                                                                                                                                                       AGCTCTATCTGGGACACCATCTTGACCAAACACCAAGAAGGCATCTACAACACCATCTGC
                                                                                                                                                                                                rgAspProSerProProProProArgThr----ArgThrProArgGln-----SerT
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                                                                                                                                                                                                                                                       287 hrHisThrProProHisProThrThrThrArg------
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                                                           CTGGGAGTCCTCCTGGGCCTGCCACTCTTGGTGA
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The invention relates to an isolated polymuclectide (ACF64435-ACF64733)

canoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymuclectide of the invention; and invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared polymetries and insolated T cell population comprising P. acnes polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit can detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymuclectides, antibodies, fusion patient, and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymeptides are useful for diagnosing, preventing or treating acnes to relating an immune response against P. acnes or primers for moteic acid hybridistation; and mamune response against P. acnes, or for treating acnes to sequence represents a specifically claimed P. acnes, or for treating and the kit is useful for performing a diagnostic assay. The present compassion of an immunogenic region. Note: The sequence date for this patent did not form part of the printed specification, but was the present sequence in electronic format directly from WIPO at New Propionibacterium acmes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acme vulgaris, or for stimulating an immune response specific for a P. acmes protein. Carter D; Maisonneuve JL; Jones R, Carte 487 1102 48 1129 172 25 Bhatia A, Benson DR, Matches: Conservative: Mismatches: Claim 7; SEQ ID NO 29447; 1481pp; English Indels: obtained in electronic format directly fr ftp.wipo.int/pub/published_pct_sequences Skeiky YAW, Persing DH, 19 S, Jen S, Lodes MJ, Wang S, Jen S, Lode Vallieve-Douglass J; 118.00 33.33% 22.67% 1.47% WPI; 2003-381789/36 Best Local Similarity: Sequence 487 AA; Percent Similarity: Alignment Scores: Mitcham JL, Zhang Y, Barth B, Query Match:

US-10-776-827-10 (1-4460) x ABM64771 (1-487)

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| e | 356 | 356 TACAAGTGGTCAAGGTTGCATCCTTTTGAGCTCAGGACCTGCTTGTAAGCCGAGAGGGTT 415 |
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| 4 | 116 | 416 CTCTGGCCCTAATCTAGCCCAAGGAGGAGAATCAGTGCCTTCTTCAGCTCTATCT 475 |
| | 22 | .:: ::: ThrProTrpLeuProSerAlaMetArgCys 31 |
| . 47 | 476 | 476 GGGACACCATCTTGACCAAACACCAAGAAGGCATCTACAACACCATCTGCCTGGGAGT 533 |
| | 32 | 32 LysGlnProSerValProArgThrIleSerSerLeuSerPheProCysTrp-SerGl 50 |
| | 534 | 548 |
| | 50 | 50 uArgThrValGlyGlyGlyGlyValValSerProProProProThrSerGlnHisLeuAr 70 |
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349 hrLeuMetGlnProProIleLeuLeuArgAsnArgLeuLeuHisLeuGlnHisGlnIleS 369
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                    rThrSerArgGlnThrThrProGlnIleIleThrArgFroThrArgThrProProThrLe
                                                                       191 erProSerThrArgHisGlnHisArgProAsnHisTyrIleArgLeuThrThrArgLeuP
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                                                                                                             GAAGAAGACCTCTGGATCTCTGCTCAACCCAAGCTTCTCCAGATGGAGAAGAGACCATCA
                                                                                                                                        targHisGlyThrargHisIleArgHisThr-----IleLysHisArgThrProHisHi
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-TIGCIGCIGGAGCCCACCAGGCAAGAGGG--
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RESULT 13

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCTGTCAGTGGCATGCCC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wer isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                         n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
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Conservative:
Mismatches:
Indels:
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                                                                                                                          Novel human diagnostic protein #8379.
                    ABG08388 standard; protein; 654 AA.
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                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
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1.47%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 654 AA;
                                                                                                                                                                                                                                               WO200175067-A2.
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                                                                                                                                                                                                                  Homo sapiens.
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                                                      ABG08388;
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| do do yo | CysSerLysPheGlySerProAlaSerSerAspAlaTrpProArgLeuGlnPro | 8 8 | |
| & 8 & | | 5 | |
| g & | 386 CTCAGGACCTGCTTGTAAGCCGAGAGGGTTCTCTGGCCCTAATCTAGCCAAGCACCATGG 445 | ÿ á | |
| ò | 207ValThrPhe 212 | 3 8 | |
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| λŏ | 491 CCAAACACCAAGAAGGGATCTACAACACCATCTG | 7 q | |
| qq | 233 ProLeuSerAsnSerAlaAlaGlnThrPro-PhePheProProLeuHisProThrAlaPr 252 | ò | 1340 AGTACTO |
| ò | | Dp | |
| Ωp | 252 oSerCysProLeuGlyLeuProGlySerProProGlyProThrSerSerThrGlyAspTy 272 | RESULT | LT 14 |
| λõ | 563 T 575 | ABP9 ID | ABP96069 ID ABP96069 standar |
| qa | 272 rlleProThr***AspGlnSerGlyThrSerLysLeuTyrCysProLeuGlnGlyGl 292 | ¥ XX | ABP96069; |
| λō | CATCTGCCATTGCTGGAGCCCACCAGGAA | XX | G7-MAY-2003 (£i |
| q | 292 yAlaGluAlaAlaHisCysValProAlaProGluGlnProGluThrAsnSerLysArgLy 312 | XX En | Human protein ki |
| ον | 612 | XX | Human; protein |
| q 0 | 312 sGlyGluThrProAsnAspLysGluGlyGluThrProAsnGluLysLy 332 | 3 X | antidiabetic; ar |
| λõ | 638 AGAAGAAGAAGAAGAAGAAGGATGAAGAAGACTCTTGGATCTCTGCTCAACCCAAGCTTC 697 | X X X | chronic obstruct |
| qq | ::: :::::::::::::::::::::::::::::: | M M M | autoimmune diso |
| ò | 698 TCCAGATGGAGAAGAGACCATCACTGCTTTAGTTAGGCAGGAAGCAGGAGGTGTTTCC 757 | X X | Homo ganione |
| qo | 343AsnThrAsnThrLys3rgLysGluGlyGlu 352 | 3 X 8 | MOSOO3000901-12 |
| ζ | 758 TITCTGGGGCTAAGCCTCCTTCTGACCACACACACACATTTCAGGAACCCTGAAATAAT 817 | XX | 402030031 A |
| qq | 353 | Z X E | |
| ò | 818 GCACTATGTCCATGTCCACAGAGTAACTACTCAACCAAGGAACAA 862 | YX XX | 24-JUN-2002; 200 |
| ୍ ଶ୍ର | 359 sLysGluLysHisGlnHhrLysArgArgArgArgAsnThrAsnThrLysArgLysGl 379 | P P P | 26-JUN-2001; 200 06-NOV-2001; 200 |
| ò | 863 ACCTCAGACTAAGTGTCCCAGTGGAGGCAGTCCCAGGGACCACGTGGACAATTCTTGGA 922 | X & | (DECO-) DECODE |
| q | : ::: ::: 379 uGlyGluThrGluProAlaGlnGlyGlyThrAsnProGlyArgValGlnGnSerPr 398 | Y I | Martinez RAM, |
| ò | 923 TACTGTCTTGGCAGCTATG | 4 H H | WPI; 2003-20142 |
| qa | 398 oAlaAlaLeu***CysPheSerTyr***SerGluCysGlyGlnAlaCysProSerAspGl 418 | X | New protein king |
| ò | 948AIAGCAAIGCICCTIACIGCAGACCAGGCAIGCCICCCAC 988 | PT | associated with |
| අු | 418 uSerAlaGlyAlaArgPheThrAlaGlySerAlaProAspLysGlyLeuProProGlyPr 438 | r P X | or cancers. |
| δλ | 989 CTGTCTCTGGCATACCCCCACATGCAAAGCACAAAGAACATTTATCCAT 1036 | PS | Claim 9; Page 7 |
| đ | 438 oSerSerTrpAlaProSerSer***HisLeulleLeuAlaThrThrVa 454 | 88 | ABZ77126 to ABZ to ABP96087. Th |
| λõ | 1037 ACAICTCAATATGGTTCCCAAGTGTGTG | នួន | antidiabetic, a |
| qu | 454 lHisLeuLeuValThrArgProCys***ProProSerClyBroSerGlyHisLe 474 | 388 | therapy. A protroat |
| δλ | 1070 GCACGTAACACACACACACACACACACAAATTCAGGTAGCAGGTA 1108 | 88 | treating a dise |
| qa , | 474 uValValGlyGlyProArgProSerAlaHisHisHisSerAspLeuLeuPhe***SerSe 494 | ຽ | (COPD), asthma, |

CCAAGTATATTCTGCTCATCAAATGGTCATTGGCTATGTACTTTGTGCAGGGAAG 1168 ATCTACAGTCACAAAATGTCTCATGGGAAAGCCTTGCCAGATTCAGACACATA 1228 AATTICCTAACCAG---CAAGGCCCCCATACACCATCTATT---GCATAAACCAC 1282 TACAGAIGCA---IGCTTTCCTATTTCTAACTCTACACATAAACTTTTACTGGA 1339 ||||||| ::: ||| ||| ||| ::: ||| ||| copheproGlyGlupheGlnGluAlaHisAlaProProValGlnProSerThrAl 545 ::
ctlylleLeuArgProArgGlyArgAlaSerGlyAlaProGlySerAlaThr-- 526 ---- 554 n kinase; enzyme; antiasthmatic; antiinflammatory; antiparkinsonian; antimigraine; cardiant; cytostatic; iive; vulnerary; gene therapy; COPD; aethma; migraine; retive pullmonary disease; non-insulin dependent diabetes; sease; myocardial infarction; inflammatory bowel disease; sorder; allografit rejection; graft versus host disease; emia; wound granulation. CATAATTGGACATTCCAGCAACCTGCTACAGTCCCCACCC 1385 :::||| |||| ----LeuGlyAlaSerGlyGlyProArgGlnHisProPro 566 yLysProAspSerTrpProCysTrpThrMet--erLeuProAlaProCysLeuPro ard; protein; 1078 AA. kinase SEQ ID NO:44. Sigurdsson GT; 002WO-IB002358. 001US-0301098P. GENETICS EHF. First entry) 29/19.

New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection or cancers.

Claim 9; Page 71-72; 258pp; English.

AB277126 to AB277165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antiinflammatory, antidabetic, antiparkinsonian, antimigrathe, cardiant, cytostatic, immunosuppressive and vulnerary activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's diseases

| ខ្លួ | migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers | ::: Db 798 HisThrArgAspThrHisHisG |
|----------------------------|---|--|
| 8 % % | (e.g. leuxaemias) or wound granulation Sequence 1078 AA; | Qy 903CCACGTGGACAATTCTTGG |
| Aligr Pred. | ent Scores: 0.0439 Length: | 954 |
| Score: Percen Best L | t Similarity: 30.74% coal Similarity: 20.87% | Db 829ProGlyThr- |
| Ouer) DB: | 1.47% Indels: 6 Gaps: | 836 ArgAspAl |
| US-1(| -10 (1-4460) x ABP96069 (1-1078) | Qy 1068 ATGCACGTAACACACACACACACA |
| ð í | 222 GCCGAGATCCCCTGACGCAAAGCAAGGAAGGAAGGAAGGA | Db 856 ThrHisThrThrHisThrHisThrMetA |
| g ; | | Qy 1116 AAGTATATTCTGCTCATCAAATGGTCAT |
| S 8 | | 873 |
| ò | CTGGAAGAGGAATAAATTACAAG | 1176 |
| 2 G | | Db 885 AsnMetGlyThrHisAsnThrHisHisLisL |
| δ | 396 GCTTGTAAGCCGACAGGGTTCTCTGGCCCTAATCTAGCCAAGCAAG | √ |
| QC | 594 ThrThrGlnProHisGlyLeuTrpAlaSerSerSerArgCysProIleCysProAlaS 613 | 1230 |
| ò | 443TGGAGAGAATCAGTGCCTTCTTCAGCTCTATCTGGGACACCATCTT 488 | 925 |
| qq | 613 erSerAlaTrpAlaGlnSerSerProGlnAspThrValGlnAspAlaGlnThrProArgA 633 | 1266 |
| δλ | 489 GACCAAGAAGAAGGCATCTACAACACCA | 945 |
| Ωp | 633 laArgGlyThrGlySerAlaGlyIleProbroProGlyProThrProHisArgValPheC 653 | 1311 |
| λō | TCTGCCTGGGAGTGCCTCCTGGGCCTGCC | ::: |
| qq | snGlnAlaProGlyGlnAspSerLeuTrpValGlySerArgValH | ŢĞ. |
| ٥y | ACTCTIGGIGATCATCACACTCCTCTTCATCTGTIGCCATIGCTGCTGGAGCCCACCAGG | Db 985 ThrHisGlnThrProAsnIleIleS |
| qq | 69 | crcaccr |
| δλ. | CAAGAGGGCCA | ::: Db 1004 SerProSerLeuCys 1008 |
| ag a | hrHisThrArgAspAlaHisHisThrHisGlnGlyHisProHisThrFroArginrHisT /1 | RESULT 15 |
| ð í | 621 GCAGCCAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA | ABUS4581 ID ABUS4581 standard; protein; 1251 AA. |
| g (| hrThrHisThrArgAspinrHisThrHisGinGlyArginrFroHisThrFroGlyInr- | AC ABUS4581; |
| ð f | 68I IGCICAACCCAAGCIICICCAGAIGGAGAAGAACACAL | DAY 03-JUN-2003 (first entry) |
| 3 8 | CONTROLL STILL TO THE STIL | Human NOVX polypeptide |
| g a | ::: isThrargaspalaTyrHisThrHisGlnGlyProThrHisThrProGlyThrHisThrH | Human; NOVX; m hypertension; |
| ò | G | atrial septal defect; atrioventri pulmonary stenosis; subaortic ste |
| g | 768 isSerArgAspAlaHisHisThrHis-Gln 777 | KW tuberous scienosis; scienoderma; acite KW obesity; anorexia; neurodegenerative KW barkingov's disease immune disorder |
| ò | 801 GGAACCCTGAAATAATGCACTATGTCCATGTCCAGAGTA 842 | |
| අු | ::: 778 GlyProProGlnThrHisThrProGlyThrHisThrHisGlnGlyHisThrHisHisThr 797 | OS Homo sapiens. |
| ò | 843 ACTACTCAACCAAGGAACAAACCTCAGACTAAGTGTCCCAGTGGAGGGCAGTCCCAGGGA 902 | PN WO200281498-A2. |

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----ACTCAGGTTACAGATGCATGCTTTCCTATT 1310
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                                                                                                                                    CCTCCCACCTGTCTCTGGCATACCCCACATGCA 1013
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                                                                                                                                                                                                                                                                                            -----AATTCAGGTAGCAGGTACGTGGGC 1115
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sGluHisThrMetAspThrGlnArgAsnThrHis 884
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|||| :::||||||| GlnGlyHisThrProGlyThrAspThrGlnGly 817
                                                          GATACTGTCTTGGCAGCTATGTGTCCAATAGCA 953
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerlach V;
n SJ, Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
Gorman L, Shennoy SG, Pena CEA, Smithson G, Burgess CE, Gerlac
Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ,
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 172; 666pp; English.
                                                                                                                                      2001US-0283512P
2001US-0283710P
2001US-02834P
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2002US-0350251P.
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Padigaru M, Shi
Anderson DW, Le
Macdougall JR, Ellerman K;
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20-APR-2001;
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18-JUN-2001;
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2820 TCTGCCTGCACCAAACCCAGGGATGTGGAAGACATCTCCCCACAAACTGCCACTGCTCACC 2879 ---TCACCCCAGGGATGAAACACCCAGAA 3170 3171 ACTCACTTCTCAGTCACTTCCACAGCCGATGACTCAGAAGAGCCAAAACCCAGAATGGGGGC 3230 3369 TCTCTTCTTTCCACTTCCTTCTCATCTTTTTCTCCATGTTTTATGCTTCTCTGATTCCCT 3428 3429 CTTCTGCCTGCACCAGACCCCAGCCCTTTATTCCTCTCCATTTTCACTCCTTCCAG 3488 2940 AGGTGGAGGCTGACAGCTGAGACGTAGTGTCAGATATGATCTAGGAGGGCGGATCACCGG 2999 ------AGGCCTCTATCTCCAGGCACAATGTCCCTGCTGTCTCCTAATCCAATGGA 3137 -----ACAGACTCCCC 3257 --- GCAGGATAGGCCCT 3308 AAACGITITIGITAAATAAACAGGIGCAIGAAAGGAGCCTAAGGCCATIGITGATAICCAC 3368 1 cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides the invention 823 tThrValAladinSerLeuLeuAlaPheSerThrSerSerSerProGlyThrProLe 843 921 935 lSerThrTyrProProSerGinLysSerSerArgAlaAlaProProTrpSerThrGlyAl 955 955 aGlyGlnProSerProProProHisLeuLeuLeuGluLeuCysLeuLeuGluThrHi 975 eProlleThrSerProProCysHisProSerProSerProPheSerProlleSerSerGl 881 CCCACTCATCAACCCCTTTGACCAGAAAGAAGCACTCTGGTTCTCTATCCCCTTGTCA 2760 CATAGAGAGTTTGTCATGGGGCCTCTGGCTGTGCCCTTCACATAACAGAATAACTTGCCA GlnCysProTrpSerSerLeuProThrThrSerProProThr------PheSer 843 uSerProGlyAsnProPheSerProGlyThrPro-----IleSerProGlyProIlePh 901 rProGluPheProValProLeuSerGlnCysProTrpSerSerLeuProThrThrSerPr 921 oProThrPhe-------SerProThrCysSerGlnValGlyThrValVa 1251 128 55 177 205 25 | ::::: :::||} | OSerThrSerSerPhePro---SerThrThrAlaAlaPro-Length: Matches: Conservative: TGACAACCTTTCCTGGCGTAACTAGAGGAGTCCCAGT--Mismatches: 3060 A----CAGCAGTCAGTTGTCATTGCCATGACA Indels: US-10-776-827-10 (1-4460) x ABU54581 (1-1251) Gaps:

| OGlnValProSerSerProSerLeuLeuProH 994 | 3508 | isValileProAlaProProHisSerProProPheLeuProArgSerProGlnIleProL 1014 | 3508 | euHisThrProProAlaLeuHisPheSerHisProProAlaHisProSerPheArgSerH 1034 | CTGGCAACCCCATGGGACCTCAGGACTGCTTGACTCATCTGGGAG 3560 | ıSerPro-ArgLeuLeuHisLeuArgSerLeuVal 1053 | GGTAAGTTCACGGGGGGACAAAAAAATGATTCCTAAAGAAGAGGCT 3605 | galuproAlaGluProLeuGluProThr 1073 | TCCTAGACCAGCACAGGCTCCAGAAAGACATCCCCTAGGCCTGGACTTCTGAGCAGCTTT 3665 | | 333AGGCCTTTCCCCATTGCTCCTTTCCCCATTGCT 3725 | | TGGGGGGGGGGGGGGGGAGAAAAGGTAGAAAAATG 3785 | | AAAGGGT 3817 | | CCAAGCTGTATAGTATTTGTCAGTATTTTTTTTTTGTAAATTTCGAACACACAC | (::: ::: ::: | AAAAATTTATTTAAATAAAATACTTTGAAAATGAAAAGTCTTGATGTAGTCGGATGGTTA 3935 | 1155 | CTTTCTTAACATTAGGTATTACCCCCACTCAGACATCACTCAGAAATGATCAATGCA 3992 | ProThrSerArgArgAsnSerLeuGlnArgS 1166 | CCCAGCCTCCCTG 4031 | ::: ::: erGluProTrpCysValProAlaIleProAlaThrGlnGluAlaGluAlaG | GTCACCGCCTTCGCCATGGTAGAGTCGTAGGTCTGAGGATGAGGAATGTGGCTGTCTCAC 4091 | ArgargLeuGlnAsnHisSerProSerA 1200 | | |
|---|----------------------|---|------|---|--|--|---|-----------------------------------|---|------|---|------|--|------|--------------|------|--|-----------------------------|---|------|--|--------------------------------------|--------------------|---|---|-----------------------------------|------------|-----------------------|
| sPheProLeuGluPro-ProPheProGlnValProSerSerPro- | CCTCTGTCCCTGAACTGCCA | | | | | | | | | | AGCCAGGCTCCGGACGGCAGCC | | | | | | | | | | : CTTTCTTAACATTAGGTATTA(| | | | | | CCTTG 4096 |) la <u>L</u> eu 1201 |
| 975 | 3489 | 994 | 3508 | 1014 | 3509 | 1034 | 3561 | 1054 | 3606 | 1074 | 3666 | 1093 | 3726 | 1106 | 3786 | 1113 | 3818 | 1133 | 3876 | 1153 | 3936 | 1156 | 3993 | 1166 | 4032 | 1183 | 4092 | 1200 |
| qu | ζŎ | qa | ò | qα | δ | qq | ò | q _Q | δò | qa | δλ | qα | ò | qu | δλ | ΩD | ò | QC | ζō | αα | ٥y | qa | Qy | qa | λō | qa | λŏ | qu |

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